

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(ii) TITLE OF INVENTION:

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street, Suite 510

(C) CITY: Boston

(D) STATE: MA

(E) \ COUNTRY: USA

(F) ~~ZIP: 02109~~

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: ASCII (text).

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) ~~CLASSIFICATION:~~

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.

(B) REGISTRATION NUMBER: 36,709

(C) REFERENCE/DOCKET NUMBER: \CPI-004DVCP3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400

(B) TELEFAX: (617) 227-5941

(i) SEOUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS
(B) LOCATION: 486..2501

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

TACACTCCTT	GCCACAGTCT	GGCAGAAAGA	ATCAAACCTTC	AGAGACTCCT	CCGGCCAGTT		60									
GTAGACACTA	TCCTTGTCAA	GTGTGCAGAT	CCAACAGCCG	CACGAGTCAG	CTGTCCATAT		120									
CTACAGTGCT	GGAACTCTGC	AAGGGCCAAG	CAGGAGAGCT	GGCGGTTGGG	AGAGAAATAC		180									
TTAAAGCTGG	GTCCATCGGG	GTTGGTGGTG	TCGATTACGT	CTTAAGTTGT	ATCCTTGGA		240									
ACCAAGCTGA	ATCAAACAAC	TGGCAAGAAC	TGCTGGGTCG	CCTCTGTCTT	ATAGACAGGT		300									
TGCTGTTGGA	ATTTCTGCT	GAATTCTATC	CTCATATTGT	CAGTACTGAT	GTCTCACAAG		360									
CTGAGCCTGT	TGAAATCAGG	TACAAGAAGC	TGCTCTCCCT	CTTAACCTTT	GCCTTGCAAT		420									
CCATTGACAA	TTCCCACTCG	ATGGTTGGCA	AGCTCTCTCG	GAGGATATAT	CTGAGCTCTG		480									
CCAGG	ATG	GTG	ACC	GCA	GTG	CCC	GCT	GTG	TTT	TCC	AAG	CTG	GTA	ACC		527
	Met	Val	Thr	Ala	Val	Pro	Ala	Val	Phe	Ser	Lys	Leu	Val	Thr		
	1				5					10						
ATG	CTT	AAT	GCT	TCT	GGC	TCC	ACC	CAC	TTC	ACC	AGG	ATG	CGC	CGG	CGT	575
Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	Phe	Thr	Arg	Met	Arg	Arg	Arg	
	15				20					25					30	
CTG	ATG	GCT	ATC	GCG	GAT	GAG	GTA	GAA	ATT	GCC	GAG	GTC	ATC	CAG	CTG	623
Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	Ile	Ala	Glu	Val	Ile	Gln	Leu	
				35					40					45		
GGT	GTG	GAG	GAC	ACT	GTG	GAT	GGG	CAT	CAG	GAC	AGC	TTA	CAG	GCC	GTG	671
Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His	Gln	Asp	Ser	Leu	Gln	Ala	Val	
			50					55					60			
GCC	CCC	ACC	AGC	TGT	CTA	GAA	AAC	AGC	TCC	CTT	GAG	CAC	ACA	GTC	CAT	719
Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser	Ser	Leu	Glu	His	Thr	Val	His	
		65					70					75				
AGA	GAG	AAA	ACT	GGA	AAA	GGA	CTA	AGT	GCT	ACG	AGA	CTG	AGT	GCC	AGC	767
Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser	Ala	Thr	Arg	Leu	Ser	Ala	Ser	
	80					85				90						

TCG Ser 95	GAG Glu	GAC Asp	ATT Ile	TCT Ser	GAC Asp 100	AGA Arg	CTG Leu	GCC Ala	GGC Gly	GTC Val 105	TCT Ser	GTA Val	GGA Gly	CTT Leu	CCC Pro 110	815
AGC Ser	TCA Ser	ACA Thr	ACA Thr	ACA Thr 115	GAA Glu	CAA Gln	CCA Pro	AAG Lys	CCA Pro 120	GCG Ala	GTT Val	CAA Gln	ACA Thr	AAA Lys 125	GGC Gly	863
AGA Arg	CCC Pro	CAC His	AGT Ser 130	CAG Gln	TGT Cys	TTG Leu	AAC Asn 135	TCC Ser	TCC Ser	CCT Pro	TTG Leu	TCT Ser	CAT His 140	GCT Ala	CAA Gln	911
TTA Leu	ATG Met	TTC Phe 145	CCA Pro	GCA Ala	CCA Pro	TCA Ser	GCC Ala 150	CCT Pro	TGT Cys	TCC Ser	TCT Ser	GCC Ala 155	CCG Pro	TCT Ser	GTC Val	959
CCA Pro 160	GAT Asp	ATT Ile	TCT Ser	AAG Lys	CAC His	AGA Arg 165	CCC Pro	CAG Gln	GCA Ala	TTT Phe 170	GTT Val	CCC Pro	TGC Cys	AAA Lys	ATA Ile	1007
CCT Pro 175	TCC Ser	GCA Ala	TCT Ser	CCT Pro	CAG Gln 180	ACA Thr	CAG Gln	CGC Arg	AAG Lys	TTC Phe 185	TCT Ser	CTA Leu	CAA Gln	TTC Phe	CAG Gln 190	1055
AGG Arg	AAC Asn	TGC Cys	TCT Ser 195	GAA Glu	CAC His	CGA Arg	GAC Asp	TCA Ser	GAC Asp 200	CAG Gln	CTC Leu	TCC Ser	CCA Pro	GTC Val 205	TTC Phe	1103
ACT Thr	CAG Gln	TCA Ser	AGA Arg 210	CCC Pro	CCA Pro	CCC Pro	TCC Ser	AGT Ser 215	AAC Asn	ATA Ile	CAC His	AGG Arg 220	CCA Pro	AAG Lys	CCA Pro	1151
TCC Ser	CGA Arg 225	CCC Pro	GTT Val	CCG Pro	GGC Gly	AGT Ser	ACA Thr 230	AGC Ser	AAA Lys	CTA Leu	GGG Gly 235	GAC Asp	GCC Ala	ACA Thr	AAA Lys	1199
AGT Ser 240	AGC Ser	ATG Met	ACA Thr	CTT Leu	GAT Asp 245	CTG Leu	GGC Gly	AGT Ser	GCT Ala	TCC Ser 250	AGG Arg	TGT Cys	GAC Asp	GAC Asp	AGC Ser	1247
TTT Phe 255	GGC Gly	GGC Gly	GGC Gly	GGC Gly 260	AAC Asn	AGT Ser	GGC Gly	AAC Asn	GCC Ala	GTC Val 265	ATA Ile	CCC Pro	AGC Ser	GAC Asp	GAG Glu 270	1295
ACA Thr	GTG Val	TTC Phe	ACG Thr 275	CCG Pro	GTG Val	GAG Glu	GAC Asp	AAG Lys	TGC Cys 280	AGG Arg	TTA Leu	GAT Asp	GTG Val 285	AAC Asn	ACC Thr	1343
GAG Glu	CTC Leu	AAC Asn	TCC Ser 290	AGC Ser	ATC Ile	GAG Glu	GAC Asp	CTT Leu 295	CTT Leu	GAA Glu	GCA Ala	TCC Ser 300	ATG Met	CCT Pro	TCA Ser	1391
AGT Ser	GAC Asp 305	ACG Thr	ACA Thr	GTC Val	ACT Thr	TTC Phe	AAG Lys 310	TCC Ser	GAA Glu	GTC Val	GCC Ala 315	GTC Val	CTC Leu	TCT Ser	CCG Pro	1439

GAA	AAG	GCC	GAA	AAT	GAC	GAC	ACC	TAC	AAA	GAC	GAC	GTC	AAT	CAT	AAT	1487
Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	
320						325					330					
CAA	AAG	TGC	AAA	GAA	AAG	ATG	GAA	GCT	GAA	GAG	GAG	GAG	GCT	TTA	GCG	1535
Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	
335					340					345					350	
No 1																
ATC	GCC	ATG	GCG	ATG	TCA	GCG	TCT	CAG	GAT	GCC	CTC	CCC	ATC	GTC	CCT	1583
Ile	Ala	Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	
		353		355					360					365		
CAG	CTG	CAG	GTG	GAA	AAT	GGA	GAA	GAT	ATT	ATC	ATC	ATT	CAG	CAG	GAC	1631
Gln	Leu	Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	
			370					375					380			
ACA	CCA	GAA	ACT	CTT	CCA	GGA	CAT	ACC	AAA	GCG	AAA	CAG	CCT	TAC	AGA	1679
Thr	Pro	Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	
		385					390					395				
GAA	GAC	GCT	GAG	TGG	CTG	AAA	GGC	CAG	CAG	ATA	GGC	CTC	GGA	GCA	TTT	1727
Glu	Asp	Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	
	400					405					410					
TCT	TCC	TGT	TAC	CAA	GCA	CAG	GAT	GTG	GGG	ACT	GGG	ACT	TTA	ATG	GCT	1775
Ser	Ser	Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	
415					420					425					430	
GTG	AAA	CAG	GTG	ACG	TAC	GTC	AGA	AAC	ACA	TCC	TCC	GAG	CAG	GAG	GAG	1823
Val	Lys	Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	
				435					440					445		
GTG	GTG	GAA	GCG	TTG	AGG	GAA	GAG	ATC	CGG	ATG	ATG	GGT	CAC	CTC	AAC	1871
Val	Val	Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	
			450					455					460			
CAT	CCA	AAC	ATC	ATC	CGG	ATG	CTG	GGG	GCC	ACG	TGC	GAG	AAG	AGC	AAC	1919
His	Pro	Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	
		465					470					475				
TAC	AAC	CTC	TTC	ATT	GAG	TGG	ATG	GCG	GGA	GGA	TCT	GTG	GCT	CAC	CTC	1967
Tyr	Asn	Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	Ser	Val	Ala	His	Leu	
	480					485					490					
TTG	AGT	AAA	TAC	GGA	GCT	TTC	AAG	GAG	TCA	GTC	GTC	ATT	AAC	TAC	ACT	2015
Leu	Ser	Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	Val	Ile	Asn	Tyr	Thr	
495					500					505					510	
GAG	CAG	TTA	CTG	CGT	GGC	CTT	TCC	TAT	CTC	CAC	GAG	AAC	CAG	ATC	ATT	2063
Glu	Gln	Leu	Leu	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu	Asn	Gln	Ile	Ile	
	</															

AGG	CTG	AGA	ATT	GCA	GAC	TTT	GGA	GCT	GCT	GCC	AGG	TTG	GCA	TCA	AAA	2159
Arg	Leu	Arg	Ile	Ala	Asp	Phe	Gly	Ala	Ala	Ala	Arg	Leu	Ala	Ser	Lys	
		545					550					555				
GGA	ACC	GGT	GCA	GGA	GAG	TTC	CAG	GGA	CAG	TTA	CTG	GGG	ACA	ATT	GCA	2207
Gly	Thr	Gly	Ala	Gly	Glu	Phe	Gln	Gly	Gln	Leu	Leu	Gly	Thr	Ile	Ala	
		560				565					570					
TTC	ATG	GCG	CCT	GAG	GTC	CTA	AGA	GGT	CAG	CAG	TAT	GGT	AGG	AGC	TGT	2255
Phe	Met	Ala	Pro	Glu	Val	Leu	Arg	Gly	Gln	Gln	Tyr	Gly	Arg	Ser	Cys	
					580					585					590	
GAT	GTA	TGG	AGT	GTT	GGC	TGC	GCC	ATT	ATA	GAA	ATG	GCT	TGT	GCA	AAA	2303
Asp	Val	Trp	Ser	Val	Gly	Cys	Ala	Ile	Ile	Glu	Met	Ala	Cys	Ala	Lys	
				595					600					605		
CCA	CCT	TGG	AAT	GCA	GAA	AAA	CAC	TCC	AAT	CAT	CTC	GCC	TTG	ATA	TTT	2351
Pro	Pro	Trp	Asn	Ala	Glu	Lys	His	Ser	Asn	His	Leu	Ala	Leu	Ile	Phe	
			610					615					620			
AAG	ATT	GCT	AGC	GCA	ACT	ACT	GCA	CCG	TCC	ATC	CCG	TCA	CAC	CTG	TCC	2399
Lys	Ile	Ala	Ser	Ala	Thr	Thr	Ala	Pro	Ser	Ile	Pro	Ser	His	Leu	Ser	
		625					630					635				
CCG	GGT	CTG	CGC	GAC	GTG	GCC	GTG	CGC	TGC	TTA	GAA	CTT	CAG	CCT	CAG	2447
Pro	Gly	Leu	Arg	Asp	Val	Ala	Val	Arg	Cys	Leu	Glu	Leu	Gln	Pro	Gln	
		640				645					650					
GAC	CGG	CCT	CCG	TCC	AGA	GAG	CTG	CTG	AAA	CAT	CCG	GTC	TTC	CGT	ACC	2495
Asp	Arg	Pro	Pro	Ser	Arg	Glu	Leu	Leu	Lys	His	Pro	Val	Phe	Arg	Thr	
					660				665						670	
ACG	TGG	TAGTTAATTG				TTCAGATCAG		CTCTAATGGA			GACAGGATAT		CGAACCGGGA			2551
Thr	Trp															
GAGAGAAAAG	AGAACTTGTG					GGCGACCATG			CCGCTAACCG			CAGCCCTCAC		GCCACTGAAC		2611
AGCCAGAAAC	GGGGCCAGCG					GGGAACCGTA			CCTAAGCATG			TGATTGACAA		ATCATGACCT		2671
GTACCTAAGC	TCGATATGCA					GACATCTACA			GCTCGTGCAG			GAACTGCACA		CCGTGCCTTT		2731
CACAGGACTG	GCTCTGGGGG					ACCAGGAAGG			CGATGGAGTT			TGCATGACTA		AAGAACAGAA		2791
GCATAAATTT	ATTTTTGGAG					CACTTTTTCA			GCTAATCAGT			ATTACCATGT		ACATCAACAT		2851
GCCCGCCACA	TTTCAAATC					AGACTGTCCC			AGATGTCAAG			ATCCACTGTG		TTTGAGTTTG		2911
TTTGCA GTTC																

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 672 AA
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Val	Thr	Ala	Val	Pro	Ala	Val	Phe	Ser	Lys	Leu	Val	Thr	Met	Leu
5				10				15							
Asn	Ala	Ser	Gly	Ser	Thr	His	Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met
20				25				30							
Ala	Ile	Ala	Asp	Glu	Val	Glu	Ile	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val
35				40				45							
Glu	Asp	Thr	Val	Asp	Gly	His	Gln	Asp	Ser	Leu	Gln	Ala	Val	Ala	Pro
50				55				60							
Thr	Ser	Cys	Leu	Glu	Asn	Ser	Ser	Leu	Glu	His	Thr	Val	His	Arg	Glu
65				70				75				80			
Lys	Thr	Gly	Lys	Gly	Leu	Ser	Ala	Thr	Arg	Leu	Ser	Ala	Ser	Ser	Glu
85				90				95							
Asp	Ile	Ser	Asp	Arg	Leu	Ala	Gly	Val	Ser	Val	Gly	Leu	Pro	Ser	Ser
100				105				110							
Thr	Thr	Thr	Glu	Gln	Pro	Lys	Pro	Ala	Val	Gln	Thr	Lys	Gly	Arg	Pro
115				120				125							
His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	His	Ala	Gln	Leu	Met
130				135				140							
Phe	Pro	Ala	Pro	Ser	Ala	Pro	Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp
145				150				155				160			
Ile	Ser	Lys	His	Arg	Pro	Gln	Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser
165				170				175							
Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn
180				185				190							
Cys	Ser	Glu	His	Arg	Asp	Ser	Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln
195				200				205							
Ser	Arg	Pro	Pro	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg
210				215				220							

Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	Ala	Thr	Lys	Ser	Ser
225							230			235					240
Met	Thr	Leu	Asp	Leu	Gly	Ser	Ala	Ser	Arg	Cys	Asp	Asp	Ser	Phe	Gly
				245					250					255	
Gly	Gly	Gly	Asn	Ser	Gly	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr	Val
			260					265					270		
Phe	Thr	Pro	Val	Glu	Asp	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr	Glu	Leu
		275					280					285			
Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp
	290					295					300				
Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys
305					310					315					320
Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	Gln	Lys
				325					330					335	
Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Ala
			340					345					350		
Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	Gln	Leu
		355					360					365			
Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	Thr	Pro
	370					375					380				
Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	Glu	Asp
385					390					395					400
Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	Ser	Ser
				405					410					415	
Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	Val	Lys
			420					425					430		
Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	Val	Val
		435					440					445			
Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	His	Pro
	450					455					460				
Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	Tyr	Asn
465					470					475					480
Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	Ser	Val	Ala	His	Leu	Leu	Ser
				485					490					495	
Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	Val	Ile	Asn	Tyr	Thr	Glu	Gln
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 5539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

48

CGG	CCT	GGT	TGC	AGC	GCA	CAA	CGC	CCG	GCG	CCC	GGT	TCC	CCG	CAT	TGC	96
Arg	Pro	Gly	Cys	Ser	Ala	Gln	Arg	Pro	Ala	Pro	Gly	Ser	Pro	His	Cys	
		20						25					30			
CCC	TGC	CCT	CCC	ACC	TGC	GCC	GCG	CGC	CCG	CCC	GCC	GCT	CCG	CGC	TCC	144
Pro	Cys	Pro	Pro	Thr	Cys	Ala	Ala	Arg	Pro	Pro	Ala	Ala	Pro	Arg	Ser	
		35					40					45				
CGG	GCC	CCG	GCC	GGG	AGG	CGC	GGC	CCC	GCT	CGC	GCC	CGC	GCC	CGC	GCC	192
Arg	Ala	Pro	Ala	Gly	Arg	Arg	Gly	Pro	Ala	Arg	Ala	Arg	Ala	Arg	Ala	
	50					55					60					
CTC	GGC	AGC	AGC	GCG	CGC	CCG	CCC	ACC	CGC	CCA	CCG	CTC	CGC	CCG	CCC	240
Leu	Gly	Ser	Ser	Ala	Arg	Pro	Pro	Thr	Arg	Pro	Pro	Leu	Arg	Pro	Pro	
	65				70					75					80	
CCC	GCG	CTC	TCC	CCG	CCC	CCT	CCC	TCC	CCC	GCA	GGC	ACG	AGC	GAA	TGT	288
Pro	Ala	Leu	Ser	Pro	Pro	Pro	Pro	Ser	Pro	Ala	Gly	Thr	Ser	Glu	Cys	
				85					90					95		
AGC	CCG	CGA	GAG	AAA	ATG	GCG	GCG	GCG	GCG	GGC	GAT	CGC	GCC	TCG	TCG	336
Ser	Pro	Arg	Glu	Lys	Met	Ala	Ala	Ala	Ala	Gly	Asp	Arg	Ala	Ser	Ser	
			100					105					110			
TCG	GGA	TTC	CCG	GGC	GCC	GCG	GCG	GCG	AGT	CCC	GAG	GCG	GGC	GGC	GGC	384
Ser	Gly	Phe	Pro	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Glu	Ala	Gly	Gly	Gly	
		115					120					125				
GGC	GGA	GGA	GGA	GGA	GCT	CTC	CAG	GGA	AGC	GGC	GCG	CCC	GCA	GCG	GGC	432
Gly	Gly	Gly	Gly	Gly	Ala	Leu	Gln	Gly	Ser	Gly	Ala	Pro	Ala	Ala	Gly	
	130					135					140					
GCG	GCG	GGG	CTG	CTG	CGG	GAG	CCT	GGC	AGC	GCG	GGG	CCG	AGC	GCG	CGG	480
Ala	Ala	Gly	Leu	Leu	Arg	Glu	Pro	Gly	Ser	Ala	Gly	Pro	Ser	Ala	Arg	
	145				150					155					160	
ACT	GGC	GGC	GGC	GGC	ACG	TGC	GCA	AAG	TGC	GGA	GTG	TGG	AGC	TGG	ACC	528
Thr	Gly	Gly	Gly	Gly	Thr	Cys	Ala	Lys	Cys	Gly	Val	Trp	Ser	Trp	Thr	
				165					170					175		
AGC	TGC	CGG	AGC	AGC	CGC	TCT	TCC	TCG	CCG	CCG	CCT	CGC	CGC	CCT	GCC	576
Ser	Cys	Arg	Ser	Ser	Arg	Ser	Ser	Ser	Pro	Pro	Pro	Arg	Arg	Pro	Ala	
			180					185					190			
CAT	CTA	CTT	CCC	GTC	GCC	GGA	GCC	CGC	GGA	CGC	GGC	TGC	AGG	AGC	GAG	624
His	Leu	Leu	Pro	Val	Ala	Gly	Ala	Arg	Gly	Arg	Gly	Cys	Arg	Ser	Glu	
		195					200					205				
TCG	CTT	CCA	GCC	CGC	GCG	GGA	CCG	CCA	CCC	CCG	GGA	GCG	GCG	AGT	CGC	672
Ser	Leu	Pro	Ala	Arg	Ala	Gly	Pro	Pro	Pro	Pro	Gly	Ala	Ala	Ser	Arg	
	210					215					220					
TGC	GGC	TCC	CAC	TCT	GCC	GAG	CTG	GCG	GCC	GCG	CGG	GAC	AGC	GGC	GCC	

CGG	AGC	CCC	GCG	GGG	GCG	GAG	CCG	CCC	TCT	GCA	GCG	GCC	CCC	TCC	GGT	768
Arg	Ser	Pro	Ala	Gly	Ala	Glu	Pro	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Gly	
			245						250					255		
CGA	GAG	ATG	GAG	AAT	AAA	GAA	ACC	CTC	AAA	GGA	CTG	CAC	AAG	ATG	GAG	816
Arg	Glu	Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Glu	
			260					265					270			
GAT	CGC	CCG	GAG	GAG	AGA	ATG	ATC	CGG	GAG	AAG	CTC	AAG	GCG	ACC	TGT	864
Asp	Arg	Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	
		275					280					285				
ATG	CCG	GCC	TGG	AAG	CAC	GAG	TGG	TTG	GAG	AGG	AGG	AAC	AGG	AGA	GGC	912
Met	Pro	Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	Asn	Arg	Arg	Gly	
	290					295				300						
CCT	GTG	GTG	GTG	AAG	CCA	ATC	CCT	ATT	AAA	GGA	GAT	GGA	TCT	GAA	GTG	960
Pro	Val	Val	Val	Lys	Pro	Ile	Pro	Ile	Lys	Gly	Asp	Gly	Ser	Glu	Val	
305				310					315					320		
AAT	AAC	TTG	GCA	GCT	GAG	CCC	CAG	GGA	GAG	GGC	CAG	GCA	GGT	TCC	GCT	1008
Asn	Asn	Leu	Ala	Ala	Glu	Pro	Gln	Gly	Glu	Gly	Gln	Ala	Gly	Ser	Ala	
			325					330					335			
GCA	CCA	GCC	CCC	AAG	GGC	CGA	CGA	AGC	CCA	TCT	CCT	GGC	AGC	TCT	CCG	1056
Ala	Pro	Ala	Pro	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Pro	
		340						345				350				
TCA	GGG	CGC	TCG	GTG	AAG	CCG	GAA	TCC	CCA	GGA	GTA	AGA	CGG	AAA	CGA	1104
Ser	Gly	Arg	Ser	Val	Lys	Pro	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	
	355					360					365					
GTG	TCC	CCG	GTG	CCT	TTC	CAG	AGT	GGC	AGA	ATC	ACA	CCA	CCC	CGA	AGA	1152
Val	Ser	Pro	Val	Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	
	370					375				380						
GCC	CCA	TCA	CCG	GAT	GGC	TTC	TCC	CCG	TAC	AGC	CCA	GAG	GAG	ACG	AGC	1200
Ala	Pro	Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Ser	
385				390				395						400		
CGC	CGC	GTG	AAC	AAA	GTG	ATG	AGA	GCC	AGG	CTG	TAC	CTG	CTG	CAG	CAG	1248
Arg	Arg	Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	
			405					410				415				
ATA	GGA	CCC	AAC	TCT	TTC	CTG	ATT	GGA	GGA	GAC	AGT	CCA	GAC	AAT	AAA	1296
Ile	Gly	Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	
		420					425			430						
TAC	CGG	GTG	TTT	ATT	GGG	CCA	CAG	AAC	TGC	AGC	TGT	GGG	CGT	GGA	GCA	1344
Tyr	Arg	Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Gly	Arg	Gly	Ala	
	435					440				445						
TTC	TGT	ATT	CAC	CTC	TTG	TTT	GTC	ATG	CTC	CGG	GTG	TTT	CAG	CTA	GAA	1392
Phe	Cys	Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	
	450					455				460						

CCC Pro 465	TCT Ser	GAC Asp	CCC Pro	ATG Met	TTA Leu	TGG Trp	AGA Arg	AAA Lys	ACT Thr	TTA Leu	AAA Lys	AAT Asn	TTC Phe	GAG Glu	GTT Val	1440
				470								480				
GAG Glu	AGT Ser	TTG Leu	TTC Phe	CAG Gln	AAA Lys	TAC Tyr	CAC His	AGT Ser	AGG Arg	CGT Arg	AGC Ser	TCG Ser	AGA Arg	ATC Ile	AAA Lys	1488
				485								495				
GCT Ala	CCA Pro	TCC Ser	CGG Arg	AAC Asn	ACC Thr	ATC Ile	CAG Gln	AAG Lys	TTT Phe	GTG Val	TCA Ser	CGC Arg	ATG Met	TCA Ser	AAT Asn	1536
				500								510				
TCT Ser	CAC His	ACA Thr	CTG Leu	TCA Ser	TCG Ser	TCT Ser	AGC Ser	ACA Thr	TCC Ser	ACA Thr	TCT Ser	AGT Ser	TCA Ser	GAA Glu	AAC Asn	1584
				515								525				
AGC Ser	ATC Ile	AAG Lys	GAT Asp	GAA Glu	GAG Glu	GAG Glu	CAG Gln	ATG Met	TGT Cys	CCC Pro	ATC Ile	TGC Cys	TTG Leu	CTG Leu	GGC Gly	1632
				530								540				
ATG Met	CTG Leu	GAT Asp	GAG Glu	GAG Glu	AGC Ser	CTG Leu	ACT Thr	GTG Val	TGT Cys	GAA Glu	GAT Asp	GGC Gly	TGC Cys	AGG Arg	AAC Asn	1680
				545								555				
AAG Lys	CTG Leu	CAC His	CAC His	CAT His	TGC Cys	ATG Met	TCC Ser	ATC Ile	TGG Trp	GCG Ala	GAA Glu	GAG Glu	TGT Cys	AGA Arg	AGA Arg	1728
				565								575				
AAT Asn	AGA Arg	GAG Glu	CCT Pro	TTA Leu	ATA Ile	TGT Cys	CCC Pro	CTT Leu	TGT Cys	AGA Arg	TCT Ser	AAG Lys	TGG Trp	AGA Arg	TCC Ser	1776
				580								590				
CAT His	GAC Asp	TTC Phe	TAC Tyr	AGC Ser	CAT His	GAG Glu	TTA Leu	TCA Ser	AGC Ser	CCC Pro	GTG Val	GAG Glu	TCC Ser	CCC Pro	GCC Ala	1824
				595								605				
TCC Ser	CTG Leu	CGA Arg	GCT Ala	GTC Val	CAG Gln	CAG Gln	CCA Pro	TCC Ser	TCC Ser	CCG Pro	CAG Gln	CAG Gln	CCC Pro	GTG Val	GCC Ala	1872
				610								620				
GGA Gly	TCA Ser	CAG Gln	CGG Arg	AGG Arg	AAT Asn	CAG Gln	GAG Glu	AGC Ser	AGT Ser	TTT Phe	AAC Asn	CTT Leu	ACT Thr	CAT His	TTT Phe	1920
				625								635				
GGA Gly	ACC Thr	CAG Gln	CAG Gln	ATT Ile	CCT Pro	TCC Ser	GCT Ala	TAC Tyr	AAA Lys	GAT Asp	TTG Leu	GCC Ala	GAG Glu	CCA Pro	TGG Trp	1968
				645								655				
ATT Ile	CAG Gln	GTG Val	TTT Phe	GGA Gly	ATG Met	GAA Glu	CTC Leu	GTT Val	GGC Gly	TGC Cys	TTA Leu	TTC Phe	TCT Ser	AGA Arg	AAC Asn	2016
				660								670				
TGG Trp	AAC Asn	GTA Val	AGG Arg	GAA Glu	ATG Met	GCC Ala	CTT Leu	AGG Arg	CGT Arg	CTT Leu	TCC Ser	CAC His	GAC Asp	GTT Val	AGT Ser	2064
				675								685				

CGG	AGG	ATA	TAT	CTG	AGC	TCT	GCC	AGG	ATG	GTG	ACC	GCA	GTG	CCC	GCT	2784
Arg	Arg	Ile	Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Ala	Val	Pro	Ala	
		915					920					925				
GTG	TTT	TCC	AAG	CTG	GTA	ACC	ATG	CTT	AAT	GCT	TCT	GGC	TCC	ACC	CAC	2832
Val	Phe	Ser	Lys	Leu	Val	Thr	Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	
		930					935				940					
TTC	ACC	AGG	ATG	CGC	CGG	CGT	CTG	ATG	GCT	ATC	GCG	GAT	GAG	GTA	GAA	2880
Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	
		945				950				955					960	
ATT	GCC	GAG	GTC	ATC	CAG	CTG	GGT	GTG	GAG	GAC	ACT	GTG	GAT	GGG	CAT	2928
Ile	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His	
				965					970					975		
CAG	GAC	AGC	TTA	CAG	GCC	GTG	GCC	CCC	ACC	AGC	TGT	CTA	GAA	AAC	AGC	2976
Gln	Asp	Ser	Leu	Gln	Ala	Val	Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser	
			980					985					990			
TCC	CTT	GAG	CAC	ACA	GTC	CAT	AGA	GAG	AAA	ACT	GGA	AAA	GGA	CTA	AGT	3024
Ser	Leu	Glu	His	Thr	Val	His	Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser	
		995					1000					1005				
GCT	ACG	AGA	CTG	AGT	GCC	AGC	TCG	GAG	GAC	ATT	TCT	GAC	AGA	CTG	GCC	3072
Ala	Thr	Arg	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Asp	Arg	Leu	Ala	
		1010					1015				1020					
GGC	GTC	TCT	GTA	GGA	CTT	CCC	AGC	TCA	ACA	ACA	ACA	GAA	CAA	CCA	AAG	3120
Gly	Val	Ser	Val	Gly	Leu	Pro	Ser	Ser	Thr	Thr	Thr	Glu	Gln	Pro	Lys	
		1025				1030				1035					1040	
CCA	GCG	GTT	CAA	ACA	AAA	GGC	AGA	CCC	CAC	AGT	CAG	TGT	TTG	AAC	TCC	3168
Pro	Ala	Val	Gln	Thr	Lys	Gly	Arg	Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	
				1045				1050						1055		
TCC	CCT	TTG	TCT	CAT	GCT	CAA	TTA	ATG	TTC	CCA	GCA	CCA	TCA	GCC	CCT	3216
Ser	Pro	Leu	Ser	His	Ala	Gln	Leu	Met	Phe	Pro	Ala	Pro	Ser	Ala	Pro	
			1060					1065					1070			
TGT	TCC	TCT	GCC	CCG	TCT	GTC	CCA	GAT	ATT	TCT	AAG	CAC	AGA	CCC	CAG	3264
Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp	Ile	Ser	Lys	His	Arg	Pro	Gln	
		1075					1080					1085				
GCA	TTT	GTT	CCC	TGC	AAA	ATA	CCT	TCC	GCA	TCT	CCT	CAG	ACA	CAG	CGC	3312
Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg	
		1090					1095				1100					
AAG	TTC	TCT	CTA	CAA	TTC	CAG	AGG	AAC	TGC	TCT	GAA	CAC	CGA	GAC	TCA	3360
Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn	Cys	Ser	Glu	His	Arg	Asp	Ser	
		1105				1110				1115					1120	
GAC	CAG	CTC	TCC	CCA	GTC	TTC	ACT	CAG	TCA	AGA	CCC	CCA	CCC	TCC	AGT	3408
Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro	Pro	Pro	Ser	Ser	
				1125					1130					1135		

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Leu	Gly	Ser	Ser	Ala	Arg	Pro	Pro	Thr	Arg	Pro	Pro	Leu	Arg	Pro	Pro	
65						70				75						80
Pro	Ala	Leu	Ser	Pro	Pro	Pro	Pro	Ser	Pro	Ala	Gly	Thr	Ser	Glu	Cys	
				85					90					95		
Ser	Pro	Arg	Glu	Lys	Met	Ala	Ala	Ala	Ala	Gly	Asp	Arg	Ala	Ser	Ser	
			100					105					110			
Ser	Gly	Phe	Pro	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Glu	Ala	Gly	Gly	Gly	
		115					120					125				
Gly	Gly	Gly	Gly	Gly	Ala	Leu	Gln	Gly	Ser	Gly	Ala	Pro	Ala	Ala	Gly	
	130					135					140					
Ala	Ala	Gly	Leu	Leu	Arg	Glu	Pro	Gly	Ser	Ala	Gly	Pro	Ser	Ala	Arg	
145					150					155					160	
Thr	Gly	Gly	Gly	Gly	Thr	Cys	Ala	Lys	Cys	Gly	Val	Trp	Ser	Trp	Thr	
				165					170					175		
Ser	Cys	Arg	Ser	Ser	Arg	Ser	Ser	Ser	Pro	Pro	Pro	Arg	Arg	Pro	Ala	
			180					185					190			
His	Leu	Leu	Pro	Val	Ala	Gly	Ala	Arg	Gly	Arg	Gly	Cys	Arg	Ser	Glu	
		195					200					205				
Ser	Leu	Pro	Ala	Arg	Ala	Gly	Pro	Pro	Pro	Pro	Gly	Ala	Ala	Ser	Arg	
	210					215					220					
Cys	Gly	Ser	His	Ser	Ala	Glu	Leu	Ala	Ala	Ala	Arg	Asp	Ser	Gly	Ala	
225					230					235					240	
Arg	Ser	Pro	Ala	Gly	Ala	Glu	Pro	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Gly	
				245					250					255		
Arg	Glu	Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Glu	
			260					265					270			
Asp	Arg	Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	
		275					280					285				
Met	Pro	Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	Asn	Arg	Arg	Gly	
	290					295					300					
Pro	Val	Val	Val	Lys	Pro	Ile	Pro	Ile	Lys	Gly	Asp	Gly	Ser	Glu	Val	
305					310					315					320	
Asn	Asn	Leu	Ala	Ala	Glu	Pro	Gln	Gly	Glu	Gly	Gln	Ala	Gly	Ser	Ala	
				325					330					335		
Ala	Pro	Ala	Pro	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Pro	
			340					345					350			
Ser	Gly	Arg	Ser	Val	Lys	Pro	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	
		355					360					365				

Val	Ser	Pro	Val	Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	
370						375					380					
Ala	Pro	Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Ser	385
385					390					395						400
Arg	Arg	Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	
			405						410					415		
Ile	Gly	Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	
			420					425					430			
Tyr	Arg	Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Gly	Arg	Gly	Ala	
		435					440					445				
Phe	Cys	Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	
450						455					460					
Pro	Ser	Asp	Pro	Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys	Asn	Phe	Glu	Val	
465					470					475					480	
Glu	Ser	Leu	Phe	Gln	Lys	Tyr	His	Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	
				485					490					495		
Ala	Pro	Ser	Arg	Asn	Thr	Ile	Gln	Lys	Phe	Val	Ser	Arg	Met	Ser	Asn	
			500					505					510			
Ser	His	Thr	Leu	Ser	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Glu	Asn	
		515					520					525				
Ser	Ile	Lys	Asp	Glu	Glu	Glu	Gln	Met	Cys	Pro	Ile	Cys	Leu	Leu	Gly	
530						535					540					
Met	Leu	Asp	Glu	Glu	Ser	Leu	Thr	Val	Cys	Glu	Asp	Gly	Cys	Arg	Asn	
545					550					555					560	
Lys	Leu	His	His	His	Cys	Met	Ser	Ile	Trp	Ala	Glu	Glu	Cys	Arg	Arg	
				565					570					575		
Asn	Arg	Glu	Pro	Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser	Lys	Trp	Arg	Ser	
			580					585					590			
His	Asp	Phe	Tyr	Ser	His	Glu	Leu	Ser	Ser	Pro	Val	Glu	Ser	Pro	Ala	
		595					600					605				
Ser	Leu	Arg	Ala	Val	Gln	Gln	Pro	Ser	Ser	Pro	Gln	Gln	Pro	Val	Ala	
	610					615					620					
Gly	Ser	Gln	Arg	Arg	Asn	Gln	Glu	Ser	Ser	Phe	Asn	Leu	Thr	His	Phe	
625					630					635					640	
Gly	Thr	Gln	Gln	Ile	Pro	Ser	Ala	Tyr	Lys	Asp	Leu	Ala	Glu	Pro	Trp	
				645					650						655	

Ile	Gln	Val	Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	Ser	Arg	Asn	
			660					665							670	
Trp	Asn	Val	Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	Asp	Val	Ser	
		675					680					685				
Gly	Ala	Leu	Leu	Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	Ser	Gly	Gly	
		690				695					700					
Gly	Ser	Gly	Gly	Ser	Leu	Ser	Ala	Gly	Ala	Ala	Ser	Gly	Ser	Ser	Gln	
705					710					715					720	
Pro	Ser	Ile	Ser	Gly	Asp	Val	Val	Glu	Ala	Cys	Cys	Ser	Val	Leu	Ser	
				725					730					735		
Ile	Val	Cys	Ala	Asp	Pro	Val	Tyr	Lys	Val	Tyr	Val	Ala	Ala	Leu	Lys	
			740					745					750			
Thr	Leu	Arg	Ala	Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	Leu	Ala	Glu	
		755					760					765				
Arg	Ile	Lys	Leu	Gln	Arg	Leu	Leu	Arg	Pro	Val	Val	Asp	Thr	Ile	Leu	
		770				775						780				
Val	Lys	Cys	Ala	Asp	Ala	Asn	Ser	Arg	Thr	Ser	Gln	Leu	Ser	Ile	Ser	
785					790					795					800	
Thr	Val	Leu	Glu	Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	Val	Gly	
				805					810					815		
Arg	Glu	Ile	Leu	Lys	Ala	Gly	Ser	Ile	Gly	Val	Gly	Gly	Val	Asp	Tyr	
			820					825					830			
Val	Leu	Ser	Cys	Ile	Leu	Gly	Asn	Gln	Ala	Glu	Ser	Asn	Asn	Trp	Gln	
		835					840					845				
Glu	Leu	Leu	Gly	Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	Glu	Phe	
		850				855					860					
Pro	Ala	Glu	Phe	Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	Gln	Ala	
865					870					875					880	
Glu	Pro	Val	Glu	Ile	Arg	Tyr	Lys	Lys	Leu	Leu	Ser	Leu	Leu	Thr	Phe	
				885					890					895		
Ala	Leu	Gln	Ser	Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	Leu	Ser	
			900					905					910			
Arg	Arg	Ile	Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Ala	Val	Pro	Ala	
		915					920					925				
Val	Phe	Ser	Lys	Leu	Val	Thr	Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	
		930				935					940					
Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	
945				950						955					960	

Ile	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His
				965					970					975	
Gln	Asp	Ser	Leu	Gln	Ala	Val	Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser
			980					985					990		
Ser	Leu	Glu	His	Thr	Val	His	Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser
		995					1000					1005			
Ala	Thr	Arg	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Asp	Arg	Leu	Ala
	1010					1015					1020				
Gly	Val	Ser	Val	Gly	Leu	Pro	Ser	Ser	Thr	Thr	Thr	Glu	Gln	Pro	Lys
1025					1030					1035					1040
Pro	Ala	Val	Gln	Thr	Lys	Gly	Arg	Pro	His	Ser	Gln	Cys	Leu	Asn	Ser
				1045					1050					1055	
Ser	Pro	Leu	Ser	His	Ala	Gln	Leu	Met	Phe	Pro	Ala	Pro	Ser	Ala	Pro
			1060					1065					1070		
Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp	Ile	Ser	Lys	His	Arg	Pro	Gln
		1075					1080					1085			
Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg
	1090					1095						1100			
Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn	Cys	Ser	Glu	His	Arg	Asp	Ser
1105					1110					1115					1120
Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro	Pro	Pro	Ser	Ser
				1125					1130					1135	
Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg	Pro	Val	Pro	Gly	Ser	Thr	Ser
			1140					1145					1150		
Lys	Leu	Gly	Asp	Ala	Thr	Lys	Ser	Ser	Met	Thr	Leu	Asp	Leu	Gly	Ser
		1155					1160					1165			
Ala	Ser	Arg	Cys	Asp	Asp	Ser	Phe	Gly	Gly	Gly	Gly	Asn	Ser	Gly	Asn
	1170					1175						1180			
Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr	Val	Phe	Thr	Pro	Val	Glu	Asp	Lys
1185					1190					1195					1200
Cys	Arg	Leu	Asp	Val	Asn	Thr	Glu	Leu	Asn	Ser	Ser	Ile	Glu	Asp	Leu
				1205					1210					1215	
Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp	Thr	Thr	Val	Thr	Phe	Lys	Ser
			1220					1225					1230		
Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr
		1235					1240					1245			

Lys	Asp	Val	Asn	His	Asn	Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	
1250						1255				1260					
Glu	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Ala	Met	Ala	Met	Ser	Ala	Ser	Gln
1265					1270					1275					1280
Asp	Ala	Leu	Pro	Ile	Val	Pro	Gln	Leu	Gln	Val	Glu	Asn	Gly	Glu	Asp
				1285					1290					1295	
Ile	Ile	Ile	Ile	Gln	Gln	Asp	Thr	Pro	Glu	Thr	Leu	Pro	Gly	His	Thr
				1300				1305					1310		
Lys	Ala	Lys	Gln	Pro	Tyr	Arg	Glu	Asp	Ala	Glu	Trp	Leu	Lys	Gly	Gln
		1315					1320					1325			
Gln	Ile	Gly	Leu	Gly	Ala	Phe	Ser	Ser	Cys	Tyr	Gln	Ala	Gln	Asp	Val
1330						1335					1340				
Gly	Thr	Gly	Thr	Leu	Met	Ala	Val	Lys	Gln	Val	Thr	Tyr	Val	Arg	Asn
1345					1350					1355					1360
Thr	Ser	Ser	Glu	Gln	Glu	Glu	Val	Val	Glu	Ala	Leu	Arg	Glu	Glu	Ile
				1365					1370					1375	
Arg	Met	Met	Gly	His	Leu	Asn	His	Pro	Asn	Ile	Ile	Arg	Met	Leu	Gly
			1380					1385					1390		
Ala	Thr	Cys	Glu	Lys	Ser	Asn	Tyr	Asn	Leu	Phe	Ile	Glu	Trp	Met	Ala
		1395					1400					1405			
Gly	Gly	Ser	Val	Ala	His	Leu	Leu	Ser	Lys	Tyr	Gly	Ala	Phe	Lys	Glu
1410						1415					1420				
Ser	Val	Val	Ile	Asn	Tyr	Thr	Glu	Gln	Leu	Leu	Arg	Gly	Leu	Ser	Tyr
1425					1430					1435					1440
Leu	His	Glu	Asn	Gln	Ile	Ile	His	Arg	Asp	Val	Lys	Gly	Ala	Asn	Leu
				1445					1450					1455	
Leu	Ile	Asp	Ser	Thr	Gly	Gln	Arg	Leu	Arg	Ile	Ala	Asp	Phe	Gly	Ala
			1460					1465					1470		
Ala	Ala	Arg	Leu	Ala	Ser	Lys	Gly	Thr	Gly	Ala	Gly	Glu	Phe	Gln	Gly
		1475					1480					1485			
Gln	Leu	Leu	Gly	Thr	Ile	Ala	Phe	Met	Ala	Pro	Glu	Val	Leu	Arg	Gly
1490						1495					1500				
Gln	Gln	Tyr	Gly	Arg	Ser	Cys	Asp	Val	Trp	Ser	Val	Gly	Cys	Ala	Ile
1505					1510					1515					1520
Ile	Glu	Met	Ala	Cys	Ala	Lys	Pro	Pro	Trp	Asn	Ala	Glu	Lys	His	Ser
				1525					1530					1535	
Asn	His	Leu	Ala	Leu	Ile	Phe	Lys	Ile	Ala	Ser	Ala	Thr	Thr	Ala	Pro
			1540					1545					1550		

Lys His Pro Val Phe Arg Thr Thr Trp
1585 1590

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 466..2325 .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGGCGGCC	GCTCTAGAAC	TAGTGGATCC	CCCGGGCTGC	AGGAATTCGG	CACGAGGGAC		60
GATCCAGCGG	CAGAGTCGCC	GCTTCCGCTT	CGCTGCTTCT	CCGGTCGGCG	ACGCGGGCCC		120
GGGGCTTCCT	TTTCATCGGC	CCAGCTTATT	CCGCGGGCCC	CGGGGCTGCA	GCTACCCAGA		180
AGCGGCGAAG	AGGCCCTGGG	CTGCGCGCCC	GCTGTCCCAT	GTGAAGCAGG	TTGGGCCTGG		240
TCCCCGGCCC	GTGCCC GGTT	GTCTGCGGCC	CTTCAGGCCT	CAGGGACCCC	CGCGAGGCGC		300
TGCTCCTGGG	GGGCGCGGTG	ACAGGCCGTG	CGGGGGCGGA	GGGGCCAGCT	CGGTGGCCTC		360
CTCTCGGCCC	TCGCGTCCGC	GATCCCGCCC	AGCGGCCGGG	CAATAAAGAA	TGTTGATGGG		420
AGAACCATTT	TCCTAATTTT	CAAATTATTG	AGCTGGTCGC	GCATA ATG GAT GAT			474
				Met Asp Asp			
				1			
CAG CAA GCT TTG AAT TCA ATC ATG CAA GAT TTG GCT GTC CTT CAT AAG							522
Gln Gln Ala Leu Asn Ser Ile Met Gln Asp Leu Ala Val Leu His Lys							
5		10		15			
CCA GTC GGC CAG CAT TAT CTT TAC AAG AAA CCA GGA AAG CAA AAC CTT							570
Pro Val Gly Gln His Tyr Leu Tyr Lys Lys Pro Gly Lys Gln Asn Leu							
20		25		30		35	

CAT	CAC	CAA	AAA	AAC	AGA	ATG	ATG	TTC	GAG	TCA	AAT	TTG	AAC	ATA	GAG	618
His	His	Gln	Lys	Asn	Arg	Met	Met	Phe	Glu	Ser	Asn	Leu	Asn	Ile	Glu	
				40					45					50		
GAG	GAA	AAA	AGG	ATC	CTG	CAG	GTT	ACT	AGA	CCA	GTT	AAA	CTA	GAA	GAC	666
Glu	Glu	Lys	Arg	Ile	Leu	Gln	Val	Thr	Arg	Pro	Val	Lys	Leu	Glu	Asp	
			55					60					65			
CTG	AGA	TCT	AAG	TCT	AAG	ATC	GCC	TTT	GGG	CAG	TCT	ATG	GAT	CTA	CAC	714
Leu	Arg	Ser	Lys	Ser	Lys	Ile	Ala	Phe	Gly	Gln	Ser	Met	Asp	Leu	His	
			70				75					80				
TAT	ACC	AAC	AAT	GAG	TTG	GTA	ATT	CCG	TTA	ACT	ACC	CAA	GAT	GAC	TTG	762
Tyr	Thr	Asn	Asn	Glu	Leu	Val	Ile	Pro	Leu	Thr	Thr	Gln	Asp	Asp	Leu	
	85					90					95					
GAC	AAA	GCT	GTG	GAA	CTG	CTG	GAT	CGC	AGT	ATT	CAC	ATG	AAG	AGT	CTC	810
Asp	Lys	Ala	Val	Glu	Leu	Leu	Asp	Arg	Ser	Ile	His	Met	Lys	Ser	Leu	
100					105				110						115	
AAG	ATA	TTA	CTT	GTA	GTA	AAT	GGG	AGT	ACA	CAG	GCT	ACT	AAT	TTA	GAA	858
Lys	Ile	Leu	Leu	Val	Val	Asn	Gly	Ser	Thr	Gln	Ala	Thr	Asn	Leu	Glu	
				120					125					130		
CCA	TCA	CCG	TCA	CCA	GAA	GAT	TTG	AAT	AAT	ACA	CCA	CTT	GGT	GCA	GAG	906
Pro	Ser	Pro	Ser	Pro	Glu	Asp	Leu	Asn	Asn	Thr	Pro	Leu	Gly	Ala	Glu	
			135					140					145			
AGG	AAA	AAG	CGG	CTA	TCT	GTA	GTA	GGT	CCC	CCT	AAT	AGG	GAT	AGA	AGT	954
Arg	Lys	Lys	Arg	Leu	Ser	Val	Val	Gly	Pro	Pro	Asn	Arg	Asp	Arg	Ser	
		150					155					160				
TCC	CCT	CCT	CCA	GGA	TAC	ATT	CCA	GAC	ATA	CTA	CAC	CAG	ATT	GCC	CGG	1002
Ser	Pro	Pro	Pro	Gly	Tyr	Ile	Pro	Asp	Ile	Leu	His	Gln	Ile	Ala	Arg	
	165					170					175					
AAT	GGG	TCA	TTC	ACT	AGC	ATC	AAC	AGT	GAA	GGA	GAG	TTC	ATT	CCA	GAG	1050
Asn	Gly	Ser	Phe	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe	Ile	Pro	Glu	
180					185				190						195	
AGC	ATG	GAC	CAA	ATG	CTG	GAT	CCA	TTG	TCT	TTA	AGC	AGC	CCT	GAA	AAT	1098
Ser	Met	Asp	Gln	Met	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Ser	Pro	Glu	Asn	
				200				205						210		
TCT	GGC	TCA	GGA	AGC	TGT	CCG	TCA	CTT	GAT	AGT	CCT	TTG	GAT	GGA	GAA	1146
Ser	Gly	Ser	Gly	Ser	Cys	Pro	Ser	Leu	Asp	Ser	Pro	Leu	Asp	Gly	Glu	
			215				220						225			
AGC	TAC	CCA	AAA	TCA	CGG	ATG	CCT	AGG	GCA	CAG	AGC	TAC	CCA	GAT	AAT	1194
Ser	Tyr	Pro	Lys	Ser	Arg	Met	Pro	Arg	Ala	Gln	Ser	Tyr	Pro	Asp	Asn	
		230					235					240				
CAT	CAG	GAG	TTT	ACA	GAC</											

AAA Lys 260	GGA Gly	GGA Gly	ACA Thr	TAT Tyr	CCA Pro 265	AGA Arg	AGG Arg	TAC Tyr	CAC His	GTT Val 270	TCC Ser	TAT Tyr	CAT His	CAC His	CAG Gln 275	1290
GAG Glu	TAT Tyr	AAT Asn	GAC Asp	GGT Gly 280	CGG Arg	AAG Lys	ACT Thr	TTT Phe	CCA Pro 285	AGA Arg	GCT Ala	AGA Arg	AGG Arg	ACC Thr 290	CAG Gln	1338
GGC Gly	ACC Thr	AGT Ser	TTC Phe 295	CGG Arg	TCT Ser	CCT Pro	GTG Val	AGC Ser 300	TTC Phe	AGT Ser	CCT Pro	ACT Thr	GAT Asp 305	CAC His	TCC Ser	1386
TTA Leu	AGC Ser	ACT Thr 310	AGT Ser	AGT Ser	GGA Gly	AGC Ser	AGT Ser 315	GTC Val	TTT Phe	ACC Thr	CCA Pro	GAG Glu 320	TAT Tyr	GAC Asp	GAC Asp	1434
AGT Ser 325	CGA Arg	ATA Ile	AGA Arg	AGA Arg	CGG Arg	GGG Gly 330	AGT Ser	GAC Asp	ATA Ile	GAC Asp 335	AAT Asn	CCT Pro	ACT Thr	TTG Leu	ACT Thr	1482
GTC Val 340	ACA Thr	GAC Asp	ATC Ile	AGC Ser	CCA Pro 345	CCC Pro	AGC Ser	CGT Arg	TCA Ser	CCT Pro 350	CGA Arg	GCT Ala	CCG Pro	ACC Thr	AAC Asn 355	1530
TGG Trp	AGA Arg	CTG Leu	GGC Gly 360	AAG Lys	CTG Leu	CTT Leu	GGC Gly	CAA Gln 365	GGA Gly	GCT Ala	TTT Phe	GGT Gly	AGG Arg	GTC Val 370	TAC Tyr	1578
CTC Leu	TGC Cys	TAT Tyr	GAT Asp 375	GTT Val	GAT Asp	ACC Thr	GGA Gly	AGA Arg 380	GAG Glu	CTG Leu	GCT Ala	GTT Val	AAG Lys 385	CAA Gln	GTT Val	1626
CAG Gln	TTT Phe 390	AAC Asn	CCT Pro	GAG Glu	AGC Ser	CCA Pro	GAG Glu 395	ACC Thr	AGC Ser	AAG Lys	GAA Glu 400	GTA Val	AAT Asn	GCA Ala	CTT Leu	1674
GAG Glu 405	TGT Cys	GAA Glu	ATT Ile	CAG Gln	TTG Leu	TTG Leu	AAA Lys 410	AAC Asn	TTG Leu	TTG Leu 415	CAT His	GAG Glu	CGA Arg	ATT Ile	GTT Val	1722
CAG Gln 420	TAT Tyr	TAT Tyr	GGC Gly	TGT Cys	TTG Leu 425	AGG Arg	GAT Asp	CCT Pro	CAG Gln	GAG Glu 430	AAA Lys	ACA Thr	CTT Leu	TCC Ser	ATC Ile 435	1770
TTT Phe	ATG Met	GAG Glu	CTC Leu	TCG Ser 440	CCA Pro	GGG Gly	GGT Gly	TCA Ser 445	ATT Ile	AAG Lys	GAC Asp	CAA Gln	CTA Leu	AAA Lys 450	GCC Ala	1818
TAC Tyr	GGA Gly	GCT Ala	CTT Leu 455	ACT Thr	GAG Glu	AAC Asn	GTG Val	ACG Thr 460	AGG Arg	AAG Lys	TAC Tyr	ACC Thr	CGT Arg	CAG Gln 465	ATT Ile	1866
CTG Leu	GAG Glu	GGG Gly 470	GTC Val	CAT His	TAT Tyr	TTG Leu	CAT His 475	AGT Ser	AAT Asn	ATG Met	ATT Ile 480	GTC Val	CAT His	AGA Arg	GAT Asp	1914

(2) INFORMATION FOR SEO ID NO:6:

(A) LENGTH: 619 AA
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met 1	Asp	Asp	Gln	Gln	Ala	Leu	Asn	Ser	Ile	Met	Gln	Asp	Leu	Ala	Val	
			5						10			15				
Leu	His	Lys	Pro	Val	Gly	Gln	His	Tyr	Leu	Tyr	Lys	Lys	Pro	Gly	Lys	
			20						25			30				
Gln	Asn	Leu	His	His	Gln	Lys	Asn	Arg	Met	Met	Phe	Glu	Ser	Asn	Leu	
			35						40			45				
Asn	Ile	Glu	Glu	Glu	Lys	Arg	Ile	Leu	Gln	Val	Thr	Arg	Pro	Val	Lys	
			50						55			60				
Leu	Glu	Asp	Leu	Arg	Ser	Lys	Ser	Lys	Ile	Ala	Phe	Gly	Gln	Ser	Met	
			65						70			75			80	
Asp	Leu	His	Tyr	Thr	Asn	Asn	Glu	Leu	Val	Ile	Pro	Leu	Thr	Thr	Gln	
			85						90			95				
Asp	Asp	Leu	Asp	Lys	Ala	Val	Glu	Leu	Leu	Asp	Arg	Ser	Ile	His	Met	
			100						105			110				
Lys	Ser	Leu	Lys	Ile	Leu	Leu	Val	Val	Asn	Gly	Ser	Thr	Gln	Ala	Thr	
			115						120			125				
Asn	Leu	Glu	Pro	Ser	Pro	Ser	Pro	Glu	Asp	Leu	Asn	Asn	Thr	Pro	Leu	
			130						135			140				
Gly	Ala	Glu	Arg	Lys	Lys	Arg	Leu	Ser	Val	Val	Gly	Pro	Pro	Asn	Arg	
			145						150			155			160	
Asp	Arg	Ser	Ser	Pro	Pro	Pro	Gly	Tyr	Ile	Pro	Asp	Ile	Leu	His	Gln	
			165						170			175				
Ile	Ala	Arg	Asn	Gly	Ser	Phe	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe	
			180						185			190				
Ile	Pro	Glu	Ser	Met	Asp	Gln	Met	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Ser	
			195						200			205				
Pro	Glu	Asn	Ser	Gly	Ser	Gly	Ser	Cys	Pro	Ser	Leu	Asp	Ser	Pro	Leu	
			210						215			220				
Asp	Gly	Glu	Ser	Tyr	Pro	Lys	Ser	Arg	Met	Pro	Arg	Ala	Gln	Ser	Tyr	
			225						230			235			240	
Pro	Asp	Asn	His	Gln	Glu	Phe	Thr	Asp	Tyr	Asp	Asn	Pro	Ile	Phe	Glu	
			245						250			255				
Lys	Phe	Gly	Lys	Gly	Gly	Thr	Tyr	Pro	Arg	Arg	Tyr	His	Val	Ser	Tyr	
			260						265			270				
His	His	Gln	Glu	Tyr	Asn	Asp	Gly	Arg	Lys	Thr	Phe	Pro	Arg	Ala	Arg	
			275						280			285				

Arg	Thr	Gln	Gly	Thr	Ser	Phe	Arg	Ser	Pro	Val	Ser	Phe	Ser	Pro	Thr
290							295							300	
Asp	His	Ser	Leu	Ser	Thr	Ser	Ser	Gly	Ser	Ser	Val	Phe	Thr	Pro	Glu
305					310					315					320
Tyr	Asp	Asp	Ser	Arg	Ile	Arg	Arg	Arg	Gly	Ser	Asp	Ile	Asp	Asn	Pro
				325					330					335	
Thr	Leu	Thr	Val	Thr	Asp	Ile	Ser	Pro	Pro	Ser	Arg	Ser	Pro	Arg	Ala
			340					345					350		
Pro	Thr	Asn	Trp	Arg	Leu	Gly	Lys	Leu	Leu	Gly	Gln	Gly	Ala	Phe	Gly
		355					360					365			
Arg	Val	Tyr	Leu	Cys	Tyr	Asp	Val	Asp	Thr	Gly	Arg	Glu	Leu	Ala	Val
	370					375					380				
Lys	Gln	Val	Gln	Phe	Asn	Pro	Glu	Ser	Pro	Glu	Thr	Ser	Lys	Glu	Val
385					390					395					400
Asn	Ala	Leu	Glu	Cys	Glu	Ile	Gln	Leu	Leu	Lys	Asn	Leu	Leu	His	Glu
				405					410					415	
Arg	Ile	Val	Gln	Tyr	Tyr	Gly	Cys	Leu	Arg	Asp	Pro	Gln	Glu	Lys	Thr
			420					425					430		
Leu	Ser	Ile	Phe	Met	Glu	Leu	Ser	Pro	Gly	Gly	Ser	Ile	Lys	Asp	Gln
		435					440					445			
Leu	Lys	Ala	Tyr	Gly	Ala	Leu	Thr	Glu	Asn	Val	Thr	Arg	Lys	Tyr	Thr
	450					455					460				
Arg	Gln	Ile	Leu	Glu	Gly	Val	His	Tyr	Leu	His	Ser	Asn	Met	Ile	Val
465					470					475					480
His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	Arg	Asp	Ser	Thr	Gly	Asn
				485					490					495	
Ile	Lys	Leu	Gly	Asp	Phe	Gly	Ala	Ser	Lys	Arg	Leu	Gln	Thr	Ile	Cys
			500					505					510		
Leu	Ser	Gly	Thr	Gly	Met	Lys	Ser	Val	Thr	Gly	Thr	Pro	Tyr	Trp	Met
		515					520					525			
Ser	Pro	Glu	Val	Ile	Ser	Gly	Glu	Gly	Tyr	Gly	Arg	Lys	Ala	Asp	Ile
	530					535					540				
Trp	Ser	Val	Ala	Cys	Thr	Val	Val	Glu	Met	Leu	Thr	Glu	Lys	Pro	Pro
545					550					555					560
Trp	Ala	Glu	Phe	Glu	Ala	Met	Ala	Ala	Ile	Phe	Lys	Ile	Ala	Thr	Gln
				565					570					575	
Pro	Thr	Asn	Pro	Lys	Leu	Pro	Pro	His	Val	Ser	Asp	Tyr	Thr	Arg	Asp
			580					585					590		

Glu Leu Leu Arg His Met Phe Val His Tyr His
610 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 466..2325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGGCGGCC	GCTCTAGAAC	TAGTGGATCC	CCCGGGCTGC	AGGAATTCCG	CACGAGGGAC		60
GATCCAGCGG	CAGAGTCGCC	GCTTCCGCTT	CGCTGCTTCT	CCGGTCGGCG	ACGCGGGCCC		120
GGGGCTTCCT	TTTCATCGGC	CCAGCTTATT	CCGCGGGCCC	CGGGGCTGCA	GCTACCCAGA		180
AGCGGCGAAG	AGGCCCTGGG	CTGCGCGCCC	GCTGTCCCAT	GTGAAGCAGG	TTGGGCCTGG		240
TCCCCGGCCC	GTGCCC GGTT	GTCTGCGGCC	CTTCAGGCCT	CAGGGACCCC	CGCGAGGCGC		300
TGCTCCTGGG	GGGCGCGGTG	ACAGGCCGTG	CGGGGGCGGA	GGGGCCAGCT	CGGTGGCCTC		360
CTCTCGGCCC	TCGCGTCCGC	GATCCCGCCC	AGCGGCCGGG	CAATAAAGAA	TGTTGATGGG		420
AGAACCATTT	TCCTAATTTT	CAAATTATTG	AGCTGGTCGC	GCATA ATG GAT GAT			474
				Met Asp Asp			
				1			
CAG CAA GCT TTG AAT TCA ATC ATG CAA GAT TTG GCT GTC CTT CAT AAG							522
Gln Gln Ala Leu Asn Ser Ile Met Gln Asp Leu Ala Val Leu His Lys							
5			10			15	
GCC AGT CGG CCA GCA TTA TCT TTA CAA GAA ACC AGG AAA GCA AAA CCT							570
Ala Ser Arg Pro Ala Leu Ser Leu Gln Glu Thr Arg Lys Ala Lys Pro							
20			25			30	35
TCA TCA CCA AAA AAA CAG AAT GAT GTT CGA GTC AAA TTT GAA CAT AGA							618
Ser Ser Pro Lys Lys Gln Asn Asp Val Arg Val Lys Phe Glu His Arg							
			40			45	50

GGA Gly	GAA Glu	AAA Lys	AGG Arg	ATC Ile	CTG Leu	CAG Gln	GTT Val	ACT Thr	AGA Arg	CCA Pro	GTT Val	AAA Lys	CTA Leu	GAA Glu	GAC Asp	666
			55					60					65			
CTG Leu	AGA Arg	TCT Ser	AAG Lys	TCT Ser	AAG Lys	ATC Ile	GCC Ala	TTT Phe	GGG Gly	CAG Gln	TCT Ser	ATG Met	GAT Asp	CTA Leu	CAC His	714
		70					75					80				
TAT Tyr	ACC Thr	AAC Asn	AAT Asn	GAG Glu	TTG Leu	GTA Val	ATT Ile	CCG Pro	TTA Leu	ACT Thr	ACC Thr	CAA Gln	GAT Asp	GAC Asp	TTG Leu	762
	85					90					95					
GAC Asp	AAA Lys	GCT Ala	GTG Val	GAA Glu	CTG Leu	CTG Leu	GAT Asp	CGC Arg	AGT Ser	ATT Ile	CAC His	ATG Met	AAG Lys	AGT Ser	CTC Leu	810
100					105					110					115	
AAG Lys	ATA Ile	TTA Leu	CTT Leu	GTA Val	GTA Val	AAT Asn	GGG Gly	AGT Ser	ACA Thr	CAG Gln	GCT Ala	ACT Thr	AAT Asn	TTA Leu	GAA Glu	858
				120					125					130		
CCA Pro	TCA Ser	CCG Pro	TCA Ser	CCA Pro	GAA Glu	GAT Asp	TTG Leu	AAT Asn	AAT Asn	ACA Thr	CCA Pro	CTT Leu	GGT Gly	GCA Ala	GAG Glu	906
			135					140					145			
AGG Arg	AAA Lys	AAG Lys	CGG Arg	CTA Leu	TCT Ser	GTA Val	GTA Val	GGT Gly	CCC Pro	CCT Pro	AAT Asn	AGG Arg	GAT Asp	AGA Arg	AGT Ser	954
		150					155					160				
TCC Ser	CCT Pro	CCT Pro	CCA Pro	GGA Gly	TAC Tyr	ATT Ile	CCA Pro	GAC Asp	ATA Ile	CTA Leu	CAC His	CAG Gln	ATT Ile	GCC Ala	CGG Arg	1002
	165					170					175					
AAT Asn	GGG Gly	TCA Ser	TTC Phe	ACT Thr	AGC Ser	ATC Ile	AAC Asn	AGT Ser	GAA Glu	GGA Gly	GAG Glu	TTC Phe	ATT Ile	CCA Pro	GAG Glu	1050
180					185					190					195	
AGC Ser	ATG Met	GAC Asp	CAA Gln	ATG Met	CTG Leu	GAT Asp	CCA Pro	TTG Leu	TCT Ser	TTA Leu	AGC Ser	AGC Ser	CCT Pro	GAA Glu	AAT Asn	1098
				200				205						210		
TCT Ser	GGC Gly	TCA Ser	GGA Gly	AGC Ser	TGT Cys	CCG Pro	TCA Ser	CTT Leu	GAT Asp	AGT Ser	CCT Pro	TTG Leu	GAT Asp	GGA Gly	GAA Glu	1146
			215					220					225			
AGC Ser	TAC Tyr	CCA Pro	AAA Lys	TCA Ser	CGG Arg	ATG Met	CCT Pro	AGG Arg	GCA Ala	CAG Gln	AGC Ser	TAC Tyr	CCA Pro	GAT Asp	AAT Asn	1194
		230					235					240				
CAT His	CAG Gln	GAG Glu	TTT Phe	ACA Thr	GAC Asp	TAT Tyr	GAT Asp	AAC Asn	CCC Pro	ATT Ile	TTT Phe	GAG Glu	AAA Lys	TTT Phe	GGA Gly	1242
	245					250					255					

AAA Lys 260	GGA Gly 260	GGA Gly 260	ACA Thr 260	TAT Tyr 260	CCA Pro 265	AGA Arg 265	AGG Arg 265	TAC Tyr 265	CAC His 270	GTT Val 270	TCC Ser 270	TAT Tyr 270	CAT His 275	CAC His 275	CAG Gln 275	1290
GAG Glu	TAT Tyr	AAT Asn	GAC Asp	GGT Gly 280	CGG Arg 280	AAG Lys	ACT Thr	TTT Phe	CCA Pro 285	AGA Arg	GCT Ala	AGA Arg	AGG Arg	ACC Thr 290	CAG Gln 290	1338
GGC Gly	ACC Thr	AGT Ser	TTC Phe 295	CGG Arg 295	TCT Ser	CCT Pro	GTG Val	AGC Ser 300	TTC Phe	AGT Ser	CCT Pro	ACT Thr	GAT Asp 305	CAC His	TCC Ser	1386
TTA Leu	AGC Ser	ACT Thr 310	AGT Ser	AGT Ser	GGA Gly	AGC Ser	AGT Ser 315	GTC Val	TTT Phe	ACC Thr	CCA Pro	GAG Glu 320	TAT Tyr	GAC Asp	GAC Asp	1434
AGT Ser	CGA Arg 325	ATA Ile	AGA Arg	AGA Arg	CGG Arg	GGG Gly 330	AGT Ser 330	GAC Asp	ATA Ile	GAC Asp	AAT Asn 335	CCT Pro	ACT Thr	TTG Leu	ACT Thr	1482
GTC Val 340	ACA Thr	GAC Asp	ATC Ile	AGC Ser	CCA Pro 345	CCC Pro	AGC Ser	CGT Arg	TCA Ser	CCT Pro	CGA Arg	GCT Ala	CCG Pro	ACC Thr	AAC Asn 355	1530
TGG Trp	AGA Arg	CTG Leu	GGC Gly	AAG Lys 360	CTG Leu	CTT Leu	GGC Gly	CAA Gln 365	GGA Gly	GCT Ala	TTT Phe	GGT Gly	AGG Arg	GTC Val 370	TAC Tyr	1578
CTC Leu	TGC Cys	TAT Tyr	GAT Asp 375	GTT Val	GAT Asp	ACC Thr	GGA Gly 380	AGA Arg	GAG Glu	CTG Leu	GCT Ala	GTT Val	AAG Lys 385	CAA Gln	GTT Val	1626
CAG Gln	TTT Phe 390	AAC Asn	CCT Pro	GAG Glu	AGC Ser	CCA Pro	GAG Glu 395	ACC Thr	AGC Ser	AAG Lys	GAA Glu 400	GTA Val	AAT Asn	GCA Ala	CTT Leu	1674
GAG Glu 405	TGT Cys	GAA Glu	ATT Ile	CAG Gln	TTG Leu	TTG Leu	AAA Lys 410	AAC Asn	TTG Leu	TTG Leu	CAT His 415	GAG Glu	CGA Arg	ATT Ile	GTT Val	1722
CAG Gln 420	TAT Tyr	TAT Tyr	GGC Gly	TGT Cys	TTG Leu 425	AGG Arg	GAT Asp	CCT Pro	CAG Gln	GAG Glu	AAA Lys 430	ACA Thr	CTT Leu	TCC Ser	ATC Ile 435	1770
TTT Phe	ATG Met	GAG Glu	TAT Tyr 440	ATG Met	CCA Pro	GGG Gly	GGT Gly	TCA Ser 445	ATT Ile	AAG Lys	GAC Asp	CAA Gln	CTA Leu	AAA Lys 450	GCC Ala	1818
TAC Tyr	GGA Gly	GCT Ala	CTT Leu 455	ACT Thr	GAG Glu	AAC Asn	GTG Val	ACG Thr 460	AGG Arg	AAG Lys	TAC Tyr	ACC Thr	CGT Arg	CAG Gln 465	ATT Ile	1866
CTG Leu	GAG Glu	GGG Gly 470	GTC Val	CAT His	TAT Tyr	TTG Leu	CAT His 475	AGT Ser	AAT Asn	ATG Met	ATT Ile 480	GTC Val	CAT His	AGA Arg	GAT Asp	1914

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 619 AA
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:8:

Met Asp Asp Gln Gln Ala Leu Asn Ser Ile Met Gln Asp Leu Ala Val .
1 5 10 15

Leu	His	Lys	Ala	Ser	Arg	Pro	Ala	Leu	Ser	Leu	Gln	Glu	Thr	Arg	Lys
			20					25					30		
Ala	Lys	Pro	Ser	Ser	Pro	Lys	Lys	Gln	Asn	Asp	Val	Arg	Val	Lys	Phe
			35					40					45		
Glu	His	Arg	Gly	Glu	Lys	Arg	Ile	Leu	Gln	Val	Thr	Arg	Pro	Val	Lys
			50					55					60		
Leu	Glu	Asp	Leu	Arg	Ser	Lys	Ser	Lys	Ile	Ala	Phe	Gly	Gln	Ser	Met
			65					70					75		
Asp	Leu	His	Tyr	Thr	Asn	Asn	Glu	Leu	Val	Ile	Pro	Leu	Thr	Thr	Gln
			85					90					95		
Asp	Asp	Leu	Asp	Lys	Ala	Val	Glu	Leu	Leu	Asp	Arg	Ser	Ile	His	Met
			100					105					110		
Lys	Ser	Leu	Lys	Ile	Leu	Leu	Val	Val	Asn	Gly	Ser	Thr	Gln	Ala	Thr
			115					120					125		
Asn	Leu	Glu	Pro	Ser	Pro	Ser	Pro	Glu	Asp	Leu	Asn	Asn	Thr	Pro	Leu
			130					135					140		
Gly	Ala	Glu	Arg	Lys	Lys	Arg	Leu	Ser	Val	Val	Gly	Pro	Pro	Asn	Arg
			145					150					155		
Asp	Arg	Ser	Ser	Pro	Pro	Pro	Gly	Tyr	Ile	Pro	Asp	Ile	Leu	His	Gln
			165					170					175		
Ile	Ala	Arg	Asn	Gly	Ser	Phe	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe
			180					185					190		
Ile	Pro	Glu	Ser	Met	Asp	Gln	Met	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Ser
			195					200					205		
Pro	Glu	Asn	Ser	Gly	Ser	Gly	Ser	Cys	Pro	Ser	Leu	Asp	Ser	Pro	Leu
			210					215					220		
Asp	Gly	Glu	Ser	Tyr	Pro	Lys	Ser	Arg	Met	Pro	Arg	Ala	Gln	Ser	Tyr
			225					230					235		
Pro	Asp	Asn	His	Gln	Glu	Phe	Thr	Asp	Tyr	Asp	Asn	Pro	Ile	Phe	Glu
			245					250					255		
Lys	Phe	Gly	Lys	Gly	Gly	Thr	Tyr	Pro	Arg	Arg	Tyr	His	Val	Ser	Tyr
			260					265					270		
His	His	Gln	Glu	Tyr	Asn	Asp	Gly	Arg	Lys	Thr	Phe	Pro	Arg	Ala	Arg
			275					280					285		
Arg	Thr	Gln	Gly	Thr	Ser	Phe	Arg	Ser	Pro	Val	Ser	Phe	Ser	Pro	Thr
			290					295					300		

Glu Leu Leu Arg His Met Phe Val His Tyr His
610 615

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 400..2280

(xi) SEQUENCE DESCRIPTION: SEO ID NO:9:

AGGGAACAAA	AGCTGGAGCT	CCACCGCGGT	GGCGGCCCGCT	CTAGAACTAG	TGGATCCCCC		60
GGGCTGCAGG	AATTCGGCAC	GAGGAACAGT	GGCCGGTCGG	AGCGTCTTCT	GGACTTCAGG		120
ACTCGCAGGC	GGCCCGGTCTG	AGTGGCGCCG	CCGAGGCCGG	GTTGGGCCGA	GCCTGGGAGC		180
GCCGGGGATG	TAGCGGGCCA	ACCTGCTCAT	GCCACAGCGC	CCGGCCGCGG	CCGAGCCGGA		240
GCCTGGGGAG	GCGGCGGGGG	CCCCGAGCGC	AGCCACGGC	CCCCGCGCGG	AGCCAGGCCC		300
GCTGCCGTCC	CCGCCGCCCG	CTCCCCCGGC	ATGCAGCCCC	GGCTGCGGAG	GTGACACTTC		360
TGGGCTGTAG	TCGCCACCGC	CGCCTCCGCC	ATCGCCACC	ATG GAT GAA CAA GAG			414
				Met Asp Glu Gln Glu			
				1		5	
GCA TTA GAC TCG ATC ATG AAG GAC CTG GTG GCC CTC CAG ATG AGC CGA							462
Ala Leu Asp Ser Ile Met Lys Asp Leu Val Ala Leu Gln Met Ser Arg							
	10			15		20	
CGA ACC CGG TTG TCT GGA TAT GAG ACC ATG AAG AAT AAG GAC ACA GGT							510
Arg Thr Arg Leu Ser Gly Tyr Glu Thr Met Lys Asn Lys Asp Thr Gly							
	25			30		35	
CAC CCA AAC AGG CAG AGT GAC GTC AGA ATC AAG TTT GAA CAC AAT GGG							558
His Pro Asn Arg Gln Ser Asp Val Arg Ile Lys Phe Glu His Asn Gly							
	40			45		50	
GAG AGA CGA ATT ATA GCA TTC AGC CGG CCT GTG AGA TAC GAA GAT GTG							606
Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Arg Tyr Glu Asp Val							
	55			60		65	

TGTAGCGCTG	TGTCCTGGGA	AGAACTGAGA	GCCATGGACC	TGCCTTCCTT	TGAGCCCCGCC	600
TTCCTGGTGC	TCTGTGGGGT	CCTGCTGAAC	GTGATCCACG	AGTGCCTGAA	GCTGCGGGCTG	660
GAACAGAGGC	TGCCGGGGAG	CCTTCCCTCT	TGAGTATCAA	ACAGCTAGTG	CGAGAGTGTA	720
AAGAGGTCCT	AAAGGGCGGG	CTCCTG	ATG AAG CAG TAT TAC CAG TTC ATG CTG			773
			Met Lys Gln Tyr Tyr Gln Phe Met Leu			
		1		5		
CAG GAG GTC CTG GGC GGA CTG GAG AAG ACC GAC TGC AAC ATG GAT GCC						821
Gln Glu Val Leu Gly Gly Leu Glu Lys Thr Asp Cys Asn Met Asp Ala						
10		15		20	25	
TTT GAG GAG GAC CTG CAG AAG ATG CTG ATG GTG TAT TTT GAT TAC ATG						869
Phe Glu Glu Asp Leu Gln Lys Met Leu Met Val Tyr Phe Asp Tyr Met						
	30		35		40	
AGA AGC TGG ATC CAA ATG CTA CAG CAG TTA CCT CAG GCT TCC CAT AGC						917
Arg Ser Trp Ile Gln Met Leu Gln Gln Leu Pro Gln Ala Ser His Ser						
	45		50		55	
TTA AAA AAC CTG CTA GAA GAG GAA TGG AAT TTC ACC AAA GAA ATA ACC						965
Leu Lys Asn Leu Leu Glu Glu Glu Trp Asn Phe Thr Lys Glu Ile Thr						
	60		65		70	
CAT TAT ATC CGT GGC GGA GAA GCG CAG GCT GGA AAG CTT TTC TGT GAC						1013
His Tyr Ile Arg Gly Gly Glu Ala Gln Ala Gly Lys Leu Phe Cys Asp						
	75		80		85	
ATC GCA GGG ATG CTG CTG AAA TCC ACA GGG AGC TTT CTG GAA TCC GGC						1061
Ile Ala Gly Met Leu Leu Lys Ser Thr Gly Ser Phe Leu Glu Ser Gly						
90		95		100	105	
CTG CAG GAG AGC TGT GCT GAG CTG TGG ACC AGN GCC GAC GAC AAC GGT						1109
Leu Gln Glu Ser Cys Ala Glu Leu Trp Thr XAA Ala Asp Asp Asn Gly						
	110		115		120	
GCT GCC GAC GAG CTA AGG AGA TCT GTC ATC GAG ATC AGC CGA GCA CTC						1157
Ala Ala Asp Glu Leu Arg Arg Ser Val Ile Glu Ile Ser Arg Ala Leu						
	125		130		135	
AAG GAG CTC TTC CAC GAA GCC AGG GAA AGA GCC TCC AAG GCC CTG GGC						1205
Lys Glu Leu Phe His Glu Ala Arg Glu Arg Ala Ser Lys Ala Leu Gly						
	140		145		150	
TTT GCT AAA ATG CTG AGG AAG GAC CTA GAA ATA GCA GCA GAG TTC GTG						1253
Phe Ala Lys Met Leu Arg Lys Asp Leu Glu Ile Ala Ala Glu Phe Val						
	155		160		165	
CTA TCT GCA TCA GCC CGA GAG CTC CTG GAC GCT CTG AAA GCA AAG CAG						1301
Leu Ser Ala Ser Ala Arg Glu Leu Leu Asp Ala Leu Lys Ala Lys Gln						
170		175		180	185	

(2) INFORMATION FOR SEQ ID NO:12:

(A) LENGTH: 890 AA
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ix) **FEATURE:**

- (A) NAME/KEY: XAA = Any amino acid
(B) LOCATION: 116

Met Lys Gln Tyr Tyr Gln Phe Met Leu Gln Glu Val Leu Gly Gly Leu
1 5 10 15

Glu Lys Thr Asp Cys Asn Met Asp Ala Phe Glu Glu Asp Leu Gln Lys
20 25 30

Met Leu Met Val Tyr Phe Asp Tyr Met Arg Ser Trp Ile Gln Met Leu
35 40 45

Gln Gln Leu Pro Gln Ala Ser His Ser Leu Lys Asn Leu Leu Glu Glu .
50 55 60

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 127..4917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGGCTCCTG CGGCGGGCTA GAGGCGGAGG CGGAGTCGAG TCACTCCCTC ACCCGCGGGC	60
TCCTGGTCTT CCCGCACCAG GCTGCAGCTG ACGACCCGCC GCGGTCATGC GAAGCTTGAT	120
GCACGG ATG AGA GAC GCC ATC GCC GAG CCG GTG CCC CCT CCT GCC CTC	168
Met Arg Asp Ala Ile Ala Glu Pro Val Pro Pro Pro Ala Leu	
1 5 10	
GCC GAC ACC CCT GCA GCC GCC ATG GAG GAG CTG CGG CCA GCA CCG CCG	216
Ala Asp Thr Pro Ala Ala Ala Met Glu Glu Leu Arg Pro Ala Pro Pro	
15 20 25 30	
CCA CAG CCC GAG CCG GAT CCG GAG TGC TGC CCA GCG GCG AGG CAG GAG	264
Pro Gln Pro Glu Pro Asp Pro Glu Cys Cys Pro Ala Ala Arg Gln Glu	
35 40 45	
TGC ATG TTG GGA GAG TCG GCT CGC AAA AGT ATG GAA TCC GAT CCA GAG	312
Cys Met Leu Gly Glu Ser Ala Arg Lys Ser Met Glu Ser Asp Pro Glu	
50 55 60	
GAC TTT TCT GAT GAA ACA AAT ACA GAG ACT CTC TAC GGC ACC TCA CCC	360
Asp Phe Ser Asp Glu Thr Asn Thr Glu Thr Leu Tyr Gly Thr Ser Pro	
65 70 75	
CCA AGC ACA CCT CGA CAG ATG AAA CGC CTG TCA GCC AAG CAC CAG AGG	408
Pro Ser Thr Pro Arg Gln Met Lys Arg Leu Ser Ala Lys His Gln Arg	
80 85 90	
AAC AGC GCA GGG AGG CCG GCC AGC CGA TCG AAC TTG AAA GAA AAA ATG	456
Asn Ser Ala Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu Lys Met	
95 100 105 110	
AAC ACA CCG AGT CAG TCT CCA CAT AAA GAT TTG GGG AAG GGA GTG GAG	504
Asn Thr Pro Ser Gln Ser Pro His Lys Asp Leu Gly Lys Gly Val Glu	
115 120 125	
ACC GTG GAA GAA TAC AGC TAC AAG CAG GAG AAG AAG ATT CGA GCA ACT	552
Thr Val Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg Ala Thr	
130 135 140	
CTG AGA ACA ACG GAG CGA GAC CAT AAG AAA AAT GCA CAG TGC TCA TTC	600
Leu Arg Thr Thr Glu Arg Asp His Lys Lys Asn Ala Gln Cys Ser Phe	
145 150 155	

09608890-063000

ATG Met	TTG Leu	GAC Asp	TCG Ser	GTG Val	GCT Ala	GGG Gly	TCT Ser	TTG Leu	CCA Pro	AAA Lys	AAA Lys	TCG Ser	ATT Ile	CCA Pro	GAT Asp	648
160				165				170								
GTG Val	GAT Asp	CTC Leu	AAT Asn	AAG Lys	CCT Pro	TAC Tyr	CTC Leu	AGT Ser	CTC Leu	GGC Gly	TGT Cys	AGC Ser	AAT Asn	GCC Ala	AAG Lys	696
175				180				185				190				
CTG Leu	CCC Pro	GTC Val	TCG Ser	ATG Met	CCC Pro	ATG Met	CCG Pro	ATA Ile	GCC Ala	AGA Arg	ACT Thr	GCA Ala	CGG Arg	CAG Gln	ACT Thr	744
195				200				205								
TCC Ser	CGG Arg	ACT Thr	GAC Asp	TGC Cys	CCC Pro	GCA Ala	GAT Asp	CGC Arg	TTA Leu	AAG Lys	TTC Phe	TTT Phe	GAA Glu	ACA Thr	CTG Leu	792
210				215				220								
CGC Arg	CTT Leu	TTG Leu	CTA Leu	AAG Lys	CTT Leu	ACC Thr	TCA Ser	GTC Val	TCG Ser	AAG Lys	AAG Lys	AAG Lys	GAC Asp	AGG Arg	GAG Glu	840
225				230				235								
CAG Gln	AGG Arg	GGA Gly	CAA Gln	GAA Glu	AAC Asn	ACG Thr	GCT Ala	GCT Ala	TTC Phe	TGG Trp	TTC Phe	AAC Asn	CGA Arg	TCG Ser	AAC Asn	888
240				245				250								
GAA Glu	CTG Leu	ATC Ile	TGG Trp	TTA Leu	GAA Glu	CTG Leu	CAG Gln	GCC Ala	TGG Trp	CAC His	GCG Ala	GGC Gly	CGC Arg	ACC Thr	ATC Ile	936
255				260				265				270				
AAT Asn	GAC Asp	CAG Gln	GAC Asp	CTC Leu	TTT Phe	CTC Leu	TAC Tyr	ACA Thr	GCC Ala	CGC Arg	CAG Gln	GCC Ala	ATC Ile	CCA Pro	GAC Asp	984
275				280				285								
ATC Ile	ATC Ile	AAT Asn	GAG Glu	ATC Ile	CTC Leu	ACC Thr	TTC Phe	AAA Lys	GTT Val	AAC Asn	TAC Tyr	GGG Gly	AGC Ser	ATT Ile	GCC Ala	1032
290				295				300								
TTC Phe	TCC Ser	AGC Ser	AAT Asn	GGA Gly	GCC Ala	GGT Gly	TTC Phe	AAC Asn	GGG Gly	CCC Pro	TTG Leu	GTA Val	GAA Glu	GGC Gly	CAG Gln	1080
305				310				315								
TGC Cys	AGA Arg	ACC Thr	CCT Pro	CAG Gln	GAG Glu	ACA Thr	AAC Asn	CGT Arg	GTG Val	GGC Gly	TGC Cys	TCA Ser	TCG Ser	TAC Tyr	CAC His	1128
320				325				330								
GAG Glu	CAC His	CTC Leu	CAG Gln	CGC Arg	CAG Gln	AGG Arg	GTC Val	TCG Ser	TTT Phe	GAG Glu	CAG Gln	GTG Val	AAG Lys	CGG Arg	ATA Ile	1176
335				340				345				350				
ATG Met	GAG Glu	CTG Leu	CTG Leu	GAG Glu	TAC Tyr	ATG Met	GAG Glu	GCA Ala	CTT Leu	TAC Tyr	CCA Pro	TCC Ser	TTG Leu	CAG Gln	GCT Ala	1224
355				360				365								
CTG Leu	CAG Gln	AAG Lys	GAC Asp	TAT Tyr	GAA Glu	CGG Arg	TAC Tyr	GCC Ala	GCC Ala	AAG Lys	GAC Asp	TTT Phe	GAG Glu	GAC Asp	AGA Arg	1272
370				375				380								

GTG	CAG	GCG	CTC	TGC	CTG	TGG	CTC	AAC	ATC	ACG	AAA	GAT	CTA	AAT	CAG	1320
Val	Gln	Ala	Leu	Cys	Leu	Trp	Leu	Asn	Ile	Thr	Lys	Asp	Leu	Asn	Gln	
		385					390					395				
AAG	CTC	CGG	ATC	ATG	GGC	ACC	GTG	CTG	GGC	ATC	AAG	AAC	CTA	TCA	GAC	1368
Lys	Leu	Arg	Ile	Met	Gly	Thr	Val	Leu	Gly	Ile	Lys	Asn	Leu	Ser	Asp	
		400				405					410					
ATT	GGC	TGG	CCA	GTG	TTT	GAA	ATC	CCC	TCC	CCT	CGG	CCG	TCC	AAG	GGC	1416
Ile	Gly	Trp	Pro	Val	Phe	Glu	Ile	Pro	Ser	Pro	Arg	Pro	Ser	Lys	Gly	
415					420					425					430	
TAC	GAG	CCA	GAG	GAC	GAG	GTC	GAG	GAC	ACG	GAG	GTT	GAG	CTG	AGG	GAG	1464
Tyr	Glu	Pro	Glu	Asp	Glu	Val	Glu	Asp	Thr	Glu	Val	Glu	Leu	Arg	Glu	
				435				440						445		
CTG	GAG	AGC	GGG	ACG	GAG	GAG	AGT	GAC	GAG	GAG	CCA	ACC	CCC	AGT	CCG	1512
Leu	Glu	Ser	Gly	Thr	Glu	Glu	Ser	Asp	Glu	Glu	Pro	Thr	Pro	Ser	Pro	
			450					455					460			
AGG	GTG	CCA	GAG	CTC	AGG	CTG	TCC	ACA	GAC	ACC	ATC	TTG	GAC	AGT	CGC	1560
Arg	Val	Pro	Glu	Leu	Arg	Leu	Ser	Thr	Asp	Thr	Ile	Leu	Asp	Ser	Arg	
		465					470					475				
TCC	CAG	GGC	TGC	GTC	TCC	AGG	AAG	CTG	GAG	AGG	CTC	GAG	TCA	GAG	GAA	1608
Ser	Gln	Gly	Cys	Val	Ser	Arg	Lys	Leu	Glu	Arg	Leu	Glu	Ser	Glu	Glu	
		480					485				490					
GAT	TCC	ATA	GGC	TGG	GGG	ACA	GCG	GAC	TGT	GGC	CCT	GAA	GCC	AGC	AGG	1656
Asp	Ser	Ile	Gly	Trp	Gly	Thr	Ala	Asp	Cys	Gly	Pro	Glu	Ala	Ser	Arg	
495					500					505					510	
CAT	TGT	TTG	ACT	TCT	ATC	TAT	AGA	CCA	TTC	GTG	GAC	AAA	GCA	CTG	AAG	1704
His	Cys	Leu	Thr	Ser	Ile	Tyr	Arg	Pro	Phe	Val	Asp	Lys	Ala	Leu	Lys	
				515					520					525		
CAA	ATG	GGG	CTA	AGA	AAG	TTA	ATT	TTA	CGA	CTT	CAT	AAG	CTT	ATG	AAT	1752
Gln	Met	Gly	Leu	Arg	Lys	Leu	Ile	Leu	Arg	Leu	His	Lys	Leu	Met	Asn	
			530					535					540			
GGG	TCC	TTG	CAA	AGA	GCT	CGT	GTA	GCT	CTG	GTG	AAG	GAC	GAC	CGT	CCA	1800
Gly	Ser	Leu	Gln	Arg	Ala	Arg	Val	Ala	Leu	Val	Lys	Asp	Asp	Arg	Pro	
		545					550					555				
GTG	GAG	TTC	TCT	GAC	TTT	CCA	GGT	CCC	ATG	TGG	GGC	TCG	GAT	TAT	GTG	1848
Val	Glu	Phe	Ser	Asp	Phe	Pro	Gly	Pro	Met	Trp	Gly	Ser	Asp	Tyr	Val	
		560				565					570					
CAG	TTG	TCG	GGA	ACA	CCT	CCT	TCC	TCA	GAG	CAG	AAG	TGT	AGC	GCT	GTG	1896
Gln	Leu	Ser	Gly	Thr	Pro	Pro	Ser	Ser	Glu	Gln	Lys	Cys	Ser	Ala	Val	
575					580				585						590	

Thr	Pro	Ala	Ala	Ala	Met	Glu	Glu	Leu	Arg	Pro	Ala	Pro	Pro	Pro	Gln
			20					25						30	
Pro	Glu	Pro	Asp	Pro	Glu	Cys	Cys	Pro	Ala	Ala	Arg	Gln	Glu	Cys	Met
			35				40					45			
Leu	Gly	Glu	Ser	Ala	Arg	Lys	Ser	Met	Glu	Ser	Asp	Pro	Glu	Asp	Phe
		50				55					60				
Ser	Asp	Glu	Thr	Asn	Thr	Glu	Thr	Leu	Tyr	Gly	Thr	Ser	Pro	Pro	Ser
		65			70					75					80
Thr	Pro	Arg	Gln	Met	Lys	Arg	Leu	Ser	Ala	Lys	His	Gln	Arg	Asn	Ser
				85					90					95	
Ala	Gly	Arg	Pro	Ala	Ser	Arg	Ser	Asn	Leu	Lys	Glu	Lys	Met	Asn	Thr
			100					105					110		
Pro	Ser	Gln	Ser	Pro	His	Lys	Asp	Leu	Gly	Lys	Gly	Val	Glu	Thr	Val
			115				120					125			
Glu	Glu	Tyr	Ser	Tyr	Lys	Gln	Glu	Lys	Lys	Ile	Arg	Ala	Thr	Leu	Arg
		130				135					140				
Thr	Thr	Glu	Arg	Asp	His	Lys	Lys	Asn	Ala	Gln	Cys	Ser	Phe	Met	Leu
		145			150					155					160
Asp	Ser	Val	Ala	Gly	Ser	Leu	Pro	Lys	Lys	Ser	Ile	Pro	Asp	Val	Asp
				165				170					175		
Leu	Asn	Lys	Pro	Tyr	Leu	Ser	Leu	Gly	Cys	Ser	Asn	Ala	Lys	Leu	Pro
			180					185					190		
Val	Ser	Met	Pro	Met	Pro	Ile	Ala	Arg	Thr	Ala	Arg	Gln	Thr	Ser	Arg
			195				200					205			
Thr	Asp	Cys	Pro	Ala	Asp	Arg	Leu	Lys	Phe	Phe	Glu	Thr	Leu	Arg	Leu
		210				215					220				
Leu	Leu	Lys	Leu	Thr	Ser	Val	Ser	Lys	Lys	Lys	Asp	Arg	Glu	Gln	Arg
		225			230					235					240
Gly	Gln	Glu	Asn	Thr	Ala	Ala	Phe	Trp	Phe	Asn	Arg	Ser	Asn	Glu	Leu
				245				250						255	
Ile	Trp	Leu	Glu	Leu	Gln	Ala	Trp	His	Ala	Gly	Arg	Thr	Ile	Asn	Asp
			260				265						270		
Gln	Asp	Leu	Phe	Leu	Tyr	Thr	Ala	Arg	Gln	Ala	Ile	Pro	Asp	Ile	Ile
			275				280					285			
Asn	Glu	Ile	Leu	Thr	Phe	Lys	Val	Asn	Tyr	Gly	Ser	Ile	Ala	Phe	Ser
		290				295					300				

Ser	Asn	Gly	Ala	Gly	Phe	Asn	Gly	Pro	Leu	Val	Glu	Gly	Gln	Cys	Arg
305					310					315					320
Thr	Pro	Gln	Glu	Thr	Asn	Arg	Val	Gly	Cys	Ser	Ser	Tyr	His	Glu	His
				325					330					335	
Leu	Gln	Arg	Gln	Arg	Val	Ser	Phe	Glu	Gln	Val	Lys	Arg	Ile	Met	Glu
			340					345					350		
Leu	Leu	Glu	Tyr	Met	Glu	Ala	Leu	Tyr	Pro	Ser	Leu	Gln	Ala	Leu	Gln
		355					360					365			
Lys	Asp	Tyr	Glu	Arg	Tyr	Ala	Ala	Lys	Asp	Phe	Glu	Asp	Arg	Val	Gln
	370					375					380				
Ala	Leu	Cys	Leu	Trp	Leu	Asn	Ile	Thr	Lys	Asp	Leu	Asn	Gln	Lys	Leu
385					390					395					400
Arg	Ile	Met	Gly	Thr	Val	Leu	Gly	Ile	Lys	Asn	Leu	Ser	Asp	Ile	Gly
				405					410					415	
Trp	Pro	Val	Phe	Glu	Ile	Pro	Ser	Pro	Arg	Pro	Ser	Lys	Gly	Tyr	Glu
			420					425					430		
Pro	Glu	Asp	Glu	Val	Glu	Asp	Thr	Glu	Val	Glu	Leu	Arg	Glu	Leu	Glu
		435					440					445			
Ser	Gly	Thr	Glu	Glu	Ser	Asp	Glu	Glu	Pro	Thr	Pro	Ser	Pro	Arg	Val
	450					455					460				
Pro	Glu	Leu	Arg	Leu	Ser	Thr	Asp	Thr	Ile	Leu	Asp	Ser	Arg	Ser	Gln
465					470					475					480
Gly	Cys	Val	Ser	Arg	Lys	Leu	Glu	Arg	Leu	Glu	Ser	Glu	Glu	Asp	Ser
				485					490					495	
Ile	Gly	Trp	Gly	Thr	Ala	Asp	Cys	Gly	Pro	Glu	Ala	Ser	Arg	His	Cys
			500					505					510		
Leu	Thr	Ser	Ile	Tyr	Arg	Pro	Phe	Val	Asp	Lys	Ala	Leu	Lys	Gln	Met
		515					520					525			
Gly	Leu	Arg	Lys	Leu	Ile	Leu	Arg	Leu	His	Lys	Leu	Met	Asn	Gly	Ser
	530					535					540				
Leu	Gln	Arg	Ala	Arg	Val	Ala	Leu	Val	Lys	Asp	Asp	Arg	Pro	Val	Glu
545					550					555					560
Phe	Ser	Asp	Phe	Pro	Gly	Pro	Met	Trp	Gly	Ser	Asp	Tyr	Val	Gln	Leu
				565					570					575	
Ser	Gly	Thr	Pro	Pro	Ser	Ser	Glu	Gln	Lys	Cys	Ser	Ala	Val	Ser	Trp
			580					585					590		
Glu	Glu	Leu	Arg	Ala	Met	Asp	Leu	Pro	Ser	Phe	Glu	Pro	Ala	Phe	Leu
		595					600					605			

Val 610	Leu	Cys	Arg	Val	Leu	Leu	Asn	Val	Ile	His	Glu	Cys	Leu	Lys	Leu
Arg 625	Leu	Glu	Gln	Arg	Pro	Ala	Gly	Glu	Pro	Ser	Leu	Leu	Ser	Ile	Lys 640
Gln	Leu	Val	Arg	Glu 645	Cys	Lys	Glu	Val	Leu 650	Lys	Gly	Gly	Leu	Leu	Met
Lys	Gln	Tyr	Tyr 660	Gln	Phe	Met	Leu	Gln 665	Glu	Val	Leu	Gly	Gly 670	Leu	Glu
Lys	Thr	Asp 675	Cys	Asn	Met	Asp	Ala 680	Phe	Glu	Glu	Asp	Leu 685	Gln	Lys	Met
Leu 690	Met	Val	Tyr	Phe	Asp	Tyr 695	Met	Arg	Ser	Trp	Ile 700	Gln	Met	Leu	Gln
Gln 705	Leu	Pro	Gln	Ala	Ser 710	His	Ser	Leu	Lys	Asn 715	Leu	Leu	Glu	Glu	Glu 720
Trp	Asn	Phe	Thr 725	Lys	Glu	Ile	Thr	His	Tyr 730	Ile	Arg	Gly	Gly	Glu 735	Ala
Gln	Ala	Gly 740	Lys	Leu	Phe	Cys	Asp 745	Ile	Ala	Gly	Met	Leu 750	Leu	Lys	Ser
Thr	Gly 755	Ser	Phe	Leu	Glu	Ser	Gly 760	Leu	Gln	Glu	Ser	Cys 765	Ala	Glu	Leu
Trp 770	Thr	Ser	Ala	Asp	Asp	Asn 775	Gly	Ala	Ala	Asp	Glu 780	Leu	Arg	Arg	Ser
Val 785	Ile	Glu	Ile	Ser 790	Arg	Ala	Leu	Lys	Glu	Leu 795	Phe	His	Glu	Ala	Arg 800
Glu	Arg	Ala	Ser 805	Lys	Ala	Leu	Gly	Phe	Ala 810	Lys	Met	Leu	Arg	Lys 815	Asp
Leu	Glu	Ile 820	Ala	Ala	Glu	Phe	Val	Leu 825	Ser	Ala	Ser	Ala	Arg	Glu	Leu
Leu	Asp 835	Ala	Leu	Lys	Ala	Lys	Gln 840	Tyr	Val	Lys	Val	Gln 845	Ile	Pro	Gly
Leu 850	Glu	Asn	Leu	His 855	Val	Phe	Val	Pro	Asp	Ser	Leu 860	Ala	Glu	Glu	Lys
Lys 865	Ile	Ile	Leu	Gln 870	Leu	Leu	Asn	Ala	Ala	Thr 875	Gly	Lys	Asp	Cys	Ser 880
Lys	Asp	Pro	Asp 885	Asp	Val	Phe	Met	Asp	Ala 890	Phe	Leu	Leu	Leu	Thr 895	Lys

His	Gly	Asp	Arg	Ala	Arg	Glu	Thr	Val	Asp	Thr	Leu	Arg	Ser	Met	Gln	
				900					905						910	
Val	Asp	Asn	Leu	Leu	Leu	Val	Val	Gln	Val	Glu	Thr	Val	Asp	Thr	Leu	
		915					920					925				
Arg	Ser	Met	Gln	Val	Asp	Asn	Leu	Leu	Leu	Val	Val	Met	Glu	Ser	Ala	
	930					935					940					
His	Leu	Val	Leu	Gln	Arg	Lys	Ala	Phe	Gln	Gln	Ser	Ile	Glu	Gly	Leu	
945					950					955					960	
Met	Thr	Val	Arg	His	Glu	Gln	Thr	Ser	Ser	Gln	Pro	Ile	Ile	Ala	Lys	
				965					970					975		
Gly	Leu	Gln	Gln	Leu	Lys	Asn	Asp	Ala	Leu	Glu	Leu	Cys	Asn	Arg	Ile	
			980					985					990			
Ser	Asp	Ala	Ile	Asp	Arg	Val	Asp	His	Met	Phe	Thr	Leu	Glu	Phe	Asp	
		995					1000					1005				
Ala	Glu	Val	Glu	Glu	Ser	Glu	Ser	Ala	Thr	Leu	Gln	Gln	Tyr	Tyr	Arg	
	1010					1015					1020					
Glu	Ala	Met	Ile	Gln	Gly	Tyr	Asn	Ile	Gly	Phe	Glu	Tyr	His	Lys	Glu	
1025					1030					1035					1040	
Val	Val	Arg	Leu	Met	Ser	Gly	Glu	Phe	Arg	Gln	Lys	Ile	Gly	Asp	Lys	
			1045						1050					1055		
Tyr	Ile	Ser	Phe	Ala	Gln	Lys	Trp	Met	Asn	Tyr	Val	Leu	Thr	Lys	Cys	
			1060					1065					1070			
Glu	Ser	Gly	Arg	Gly	Thr	Arg	Pro	Arg	Trp	Ala	Thr	Gln	Gly	Phe	Asp	
		1075					1080					1085				
Phe	Leu	Gln	Ala	Ile	Glu	Pro	Ala	Phe	Ile	Ser	Ala	Leu	Pro	Glu	Asp	
	1090					1095					1100					
Asp	Phe	Leu	Ser	Leu	Gln	Ala	Leu	Met	Asn	Glu	Cys	Ile	Gly	His	Val	
1105					1110					1115					1120	
Ile	Gly	Lys	Pro	His	Ser	Pro	Val	Thr	Ala	Ile	His	Arg	Asn	Ser	Pro	
				1125					1130					1135		
Arg	Pro	Val	Lys	Val	Pro	Arg	Cys	His	Ser	Asp	Pro	Pro	Asn	Pro	His	
			1140					1145					1150			
Leu	Ile	Ile	Pro	Thr	Pro	Glu	Gly	Phe	Ser	Thr	Arg	Ser	Val	Pro	Ser	
		1155					1160					1165				
Asp	Ala	Arg	Thr	His	Gly	Asn	Ser	Val	Ala	Ala	Ala	Ala	Ala	Val	Arg	
	1170					1175					1180					
Ala	Ala	Ala	Thr	Thr	Ala	Ala	Gly	Arg	Pro	Gly	Pro	Gly	Gly	Gly	Asp	
1185					1190					1195					1200	

Ser Val Pro Ala Lys Pro Val Asn Thr Ala Pro Asp Thr Arg Gly Ser	1205	1210	1215
Ser Val Pro Glu Asn Asp Arg Leu Ala Ser Ile Ala Ala Glu Leu Gln	1220	1225	1230
Phe Arg Ser Leu Ser Arg His Ser Ser Pro Thr Glu Glu Arg Asp Glu	1235	1240	1245
Pro Ala Tyr Pro Arg Ser Asp Ser Ser Gly Ser Thr Arg Arg Ser Trp	1250	1255	1260
Glu Leu Arg Thr Leu Ile Ser Gln Thr Lys Asp Ser Ala Ser Lys Gln	1265	1270	1275
Gly Pro Ile Glu Ala Ile Gln Lys Ser Val Arg Leu Phe Glu Glu Arg	1285	1290	1295
Arg Tyr Arg Glu Met Arg Arg Lys Asn Ile Ile Gly Gln Val Cys Asp	1300	1305	1310
Thr Pro Lys Ser Tyr Asp Asn Val Met His Val Gly Leu Arg Lys Val	1315	1320	1325
Thr Phe Lys Trp Gln Arg Gly Asn Lys Ile Gly Glu Gly Gln Tyr Gly	1330	1335	1340
Lys Val Tyr Thr Cys Ile Ser Val Asp Thr Gly Glu Leu Met Ala Met	1345	1350	1355
Lys Glu Ile Arg Phe Gln Pro Asn Asp His Lys Thr Ile Lys Glu Thr	1365	1370	1375
Ala Asp Glu Leu Lys Ile Phe Glu Gly Ile Lys His Pro Asn Leu Val	1380	1385	1390
Arg Tyr Phe Gly Val Glu Leu His Arg Glu Glu Met Tyr Ile Phe Met	1395	1400	1405
Glu Tyr Cys Asp Glu Gly Thr Leu Glu Glu Val Ser Arg Leu Gly Leu	1410	1415	1420
Gln Glu His Val Ile Arg Leu Tyr Thr Lys Gln Ile Thr Val Ala Ile	1425	1430	1435
Asn Val Leu His Glu His Gly Ile Val His Arg Asp Ile Lys Gly Ala	1445	1450	1455
Asn Ile Phe Leu Thr Ser Ser Gly Leu Ile Lys Leu Gly Asp Phe Gly	1460	1465	1470
Cys Ser Val Lys Leu Lys Asn Asn Ala Gln Thr Met Pro Gly Glu Val	1475	1480	1485

14

Arg 1
1505

Gly

Tyr 0

Pro 1

His

Leu 1585

SUB
A2

0360490000